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(71) Applicant (for all designated States except US): **CORIXA CORPORATION** [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **XU, Jiangchun** [US/US]; 15805 SE 43rd Place, Bellevue, WA 98006

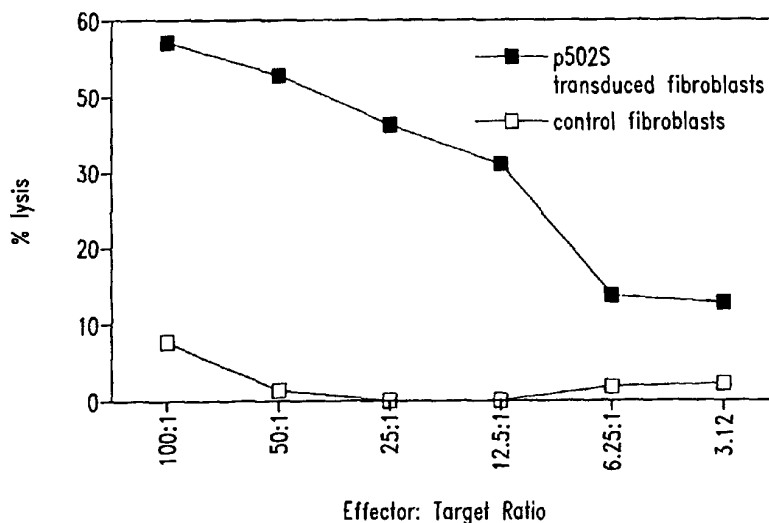
(US). **DILLON, Davin, C.** [US/US]; 18112 NW Montreux Drive, Issaquah, WA 98027 (US). **MITCHAM, Jennifer, L.** [US/US]; 16677 NE 88th Street, Redmond, WA 98052 (US). **HARLOCKER, Susan, L.** [US/US]; 7522 - 13th Avenue W., Seattle, WA 98117 (US). **JIANG, Yuqiu** [CN/US]; 5001 South 232nd Street, Kent, WA 98032 (US). **REED, Steven, G.** [US/US]; 2843 - 122nd Place NE, Bellevue, WA 98005 (US). **KALOS, Michael, D.** [US/US]; 8116 Dayton Ave. N., Seattle, WA 98103 (US). **RETTTER, Marc, W.** [US/US]; 33402 NE 43rd Place, Carnation, WA 98014 (US). **STOLK, John, A.** [US/US]; 7436 Northeast 144th Place, Bothell, WA 98011 (US). **DAY, Craig, H.** [US/US]; 11501 Stone Ave. N., C122, Seattle, WA 98133-8317 (US). **SKEIKY, Yasir, A.W.** [CA/US]; 15106 SE 47th Place, Bellevue, WA 98006 (US). **WANG, Aijun** [CN/US]; 3106 213th Place SE, Issaquah, WA 98029 (US).

(74) Agents: **POTTER, Jane, E., R.**; Seed Intellectual Property Law Group PLLC, Suite 6300, 701 Fifth Avenue, Seattle, WA 98104-7092 et al. (US).

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(54) Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER



(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer, are disclosed. Compositions may comprise one or more prostate-specific proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a prostate-specific protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as prostate cancer. Diagnostic methods based on detecting a prostate-specific protein, or mRNA encoding such a protein, in a sample are also provided.



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COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER

5 TECHNICAL FIELD

The present invention relates generally to therapy and diagnosis of cancer, such as prostate cancer. The invention is more specifically related to polypeptides comprising at least a portion of a prostate-specific protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides may be used in vaccines and pharmaceutical compositions for
10 prevention and treatment of prostate cancer, and for the diagnosis and monitoring of such cancers.

BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress
15 inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but
20 these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate
25 with prostate volume, and do not indicate the level of metastasis.

In spite of considerable research into therapies for these and other cancers, prostate cancer remains difficult to diagnose and treat effectively. Accordingly, there is a need in the art for improved methods for detecting and treating such cancers. The present invention fulfills these needs and further provides other related advantages.

30 SUMMARY OF THE INVENTION

Briefly stated, the present invention provides compositions and methods for the

diagnosis and therapy of cancer, such as prostate cancer. In one aspect, the present invention provides polypeptides comprising at least a portion of a prostate-specific protein, or a variant thereof. Certain portions and other variants are immunogenic, such that the ability of the variant to react with antigen-specific antisera is not substantially diminished. Within certain embodiments, 5 the polypeptide comprises at least an immunogenic portion of a prostate-specific protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of: (a) sequences recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382,384-476, 524, 526, 530, 531, 533, 535 and 536; (b) sequences that hybridize to any of the 10 foregoing sequences under moderately stringent conditions; and (c) complements of any of the sequence of (a) or (b). In certain specific embodiments, such a polypeptide comprises at least a portion, or variant thereof, of a protein that includes an amino acid sequence selected from the group consisting of sequences recited in any one of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-550.

15 The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least 15 amino acid residues of a prostate-specific protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions 20 comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, vaccines for prophylactic or therapeutic use are provided. Such vaccines comprise a polypeptide or polynucleotide as described above and an immunostimulant.

25 The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a prostate-specific protein; and (b) a physiologically acceptable carrier. In certain embodiments, the present invention provides monoclonal antibodies that specifically bind to an amino acid sequence selected from the group consisting of SEQ ID NO: 496, 504, 505, 509-517, 522 and 541-550, together with 30 monoclonal antibodies comprising a complementarity determining region selected from the group consisting of SEQ ID NO: 502, 503 and 506-508.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

5 Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins.

10 Within related aspects, pharmaceutical compositions comprising a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a physiologically acceptable carrier are provided.

Vaccines are further provided, within other aspects, that comprise a fusion protein, or a polynucleotide encoding a fusion protein, in combination with an immunostimulant.

15 Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as recited above.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that
20 specifically react with a prostate-specific protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described
25 above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a prostate-specific protein, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time
30 sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of a prostate-specific protein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.

10 Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody. The cancer may be prostate cancer.

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The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

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The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate-specific protein; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain

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embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that
5 hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate-specific protein; (b)
10 detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as
15 monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed
20 herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Figure 1 illustrates the ability of T cells to kill fibroblasts expressing the representative prostate-specific polypeptide P502S, as compared to control fibroblasts. The
25 percentage lysis is shown as a series of effector:target ratios, as indicated.

Figures 2A and 2B illustrate the ability of T cells to recognize cells expressing the representative prostate-specific polypeptide P502S. In each case, the number of γ -interferon spots is shown for different numbers of responders. In Figure 2A, data is presented for fibroblasts pulsed with the P2S-12 peptide, as compared to fibroblasts pulsed with a control E75 peptide. In Figure
30 2B, data is presented for fibroblasts expressing P502S, as compared to fibroblasts expressing HER-2/neu.

Figure 3 represents a peptide competition binding assay showing that the P1S#10 peptide, derived from P501S, binds HLA-A2. Peptide P1S#10 inhibits HLA-A2 restricted presentation of fluM58 peptide to CTL clone D150M58 in TNF release bioassay. D150M58 CTL is specific for the HLA-A2 binding influenza matrix peptide fluM58.

5 Figure 4 illustrates the ability of T cell lines generated from P1S#10 immunized mice to specifically lyse P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat A2Kb targets, as compared to EGFP-transduced Jurkat A2Kb. The percent lysis is shown as a series of effector to target ratios, as indicated.

Figure 5 illustrates the ability of a T cell clone to recognize and specifically lyse
10 Jurkat A2Kb cells expressing the representative prostate-specific polypeptide P501S, thereby demonstrating that the P1S#10 peptide may be a naturally processed epitope of the P501S polypeptide.

Figures 6A and 6B are graphs illustrating the specificity of a CD8⁺ cell line (3A-1) for a representative prostate-specific antigen (P501S). Figure 6A shows the results of a ⁵¹Cr release
15 assay. The percent specific lysis is shown as a series of effector:target ratios, as indicated. Figure 6B shows the production of interferon-gamma by 3A-1 cells stimulated with autologous B-LCL transduced with P501S, at varying effector:target ratios as indicated.

Figure 7 is a Western blot showing the expression of P501S in baculovirus.

Figure 8 illustrates the results of epitope mapping studies on P501S.

20 Figure 9 is a schematic representation of the P501S protein showing the location of transmembrane domains and predicted intracellular and extracellular domains.

Figure 10 is a genomic map showing the location of the prostate genes P775P, P704P, B305D, P712P and P774P within the Cat Eye Syndrome region of chromosome 22q11.2

Figure 11 shows the results of an ELISA assay of antibody specificity to P501S
25 peptides.

SEQ ID NO: 1 is the determined cDNA sequence for F1-13

SEQ ID NO: 2 is the determined 3' cDNA sequence for F1-12

SEQ ID NO: 3 is the determined 5' cDNA sequence for F1-12

SEQ ID NO: 4 is the determined 3' cDNA sequence for F1-16

30 SEQ ID NO: 5 is the determined 3' cDNA sequence for H1-1

SEQ ID NO: 6 is the determined 3' cDNA sequence for H1-9

SEQ ID NO: 7 is the determined 3' cDNA sequence for H1-4

- SEQ ID NO: 8 is the determined 3' cDNA sequence for J1-17
SEQ ID NO: 9 is the determined 5' cDNA sequence for J1-17
SEQ ID NO: 10 is the determined 3' cDNA sequence for L1-12
SEQ ID NO: 11 is the determined 5' cDNA sequence for L1-12
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SEQ ID NO: 13 is the determined 5' cDNA sequence for N1-1862
SEQ ID NO: 14 is the determined 3' cDNA sequence for J1-13
SEQ ID NO: 15 is the determined 5' cDNA sequence for J1-13
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SEQ ID NO: 28 is the determined 5' cDNA sequence for L1-14
SEQ ID NO: 29 is the determined 3' cDNA sequence for L1-14
SEQ ID NO: 30 is the determined 3' cDNA sequence for J1-12
SEQ ID NO: 31 is the determined 3' cDNA sequence for J1-16
25 SEQ ID NO: 32 is the determined 3' cDNA sequence for J1-21
SEQ ID NO: 33 is the determined 3' cDNA sequence for K1-48
SEQ ID NO: 34 is the determined 3' cDNA sequence for K1-55
SEQ ID NO: 35 is the determined 3' cDNA sequence for L1-2
SEQ ID NO: 36 is the determined 3' cDNA sequence for L1-6
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SEQ ID NO: 38 is the determined 3' cDNA sequence for N1-1860
SEQ ID NO: 39 is the determined 3' cDNA sequence for N1-1861

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- SEQ ID NO: 41 is the determined cDNA sequence for P5
- SEQ ID NO: 42 is the determined cDNA sequence for P8
- SEQ ID NO: 43 is the determined cDNA sequence for P9
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- SEQ ID NO: 48 is the determined cDNA sequence for P34
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SEQ ID NO: 95 is the determined cDNA sequence for 1H-4766
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SEQ ID NO: 104 is the determined cDNA sequence for 1D-4304

SEQ ID NO: 105 is the determined cDNA sequence for 1D-4296

SEQ ID NO: 106 is the determined cDNA sequence for 1D-4280

SEQ ID NO: 107 is the determined full length cDNA sequence for F1-12 (also referred to as P504S)

5

SEQ ID NO: 108 is the predicted amino acid sequence for F1-12

SEQ ID NO: 109 is the determined full length cDNA sequence for J1-17

SEQ ID NO: 110 is the determined full length cDNA sequence for L1-12 (also referred to as P501S)

SEQ ID NO: 111 is the determined full length cDNA sequence for N1-1862 (also referred to as

10 P503S)

SEQ ID NO: 112 is the predicted amino acid sequence for J1-17

SEQ ID NO: 113 is the predicted amino acid sequence for L1-12 (also referred to as P501S)

SEQ ID NO: 114 is the predicted amino acid sequence for N1-1862 (also referred to as P503S)

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- SEQ ID NO: 201 is the determined extended cDNA sequence for 1D.1-4278
- 5 SEQ ID NO: 202 is the determined extended cDNA sequence for 1D-4288
- SEQ ID NO: 203 is the determined extended cDNA sequence for 1D-4283
- SEQ ID NO: 204 is the determined extended cDNA sequence for 1D-4304
- SEQ ID NO: 205 is the determined extended cDNA sequence for 1D-4296
- SEQ ID NO: 206 is the determined extended cDNA sequence for 1D-4280
- 10 SEQ ID NO: 207 is the determined cDNA sequence for 10-d8fwd
- SEQ ID NO: 208 is the determined cDNA sequence for 10-H10con
- SEQ ID NO: 209 is the determined cDNA sequence for 11-C8rev
- SEQ ID NO: 210 is the determined cDNA sequence for 7.g6fwd
- SEQ ID NO: 211 is the determined cDNA sequence for 7.g6rev
- 15 SEQ ID NO: 212 is the determined cDNA sequence for 8-b5fwd
- SEQ ID NO: 213 is the determined cDNA sequence for 8-b5rev
- SEQ ID NO: 214 is the determined cDNA sequence for 8-b6fwd
- SEQ ID NO: 215 is the determined cDNA sequence for 8-b6 rev
- SEQ ID NO: 216 is the determined cDNA sequence for 8-d4fwd
- 20 SEQ ID NO: 217 is the determined cDNA sequence for 8-d9rev
- SEQ ID NO: 218 is the determined cDNA sequence for 8-g3fwd
- SEQ ID NO: 219 is the determined cDNA sequence for 8-g3rev
- SEQ ID NO: 220 is the determined cDNA sequence for 8-h11rev
- SEQ ID NO: 221 is the determined cDNA sequence for g-f12fwd
- 25 SEQ ID NO: 222 is the determined cDNA sequence for g-f3rev
- SEQ ID NO: 223 is the determined cDNA sequence for P509S
- SEQ ID NO: 224 is the determined cDNA sequence for P510S
- SEQ ID NO: 225 is the determined cDNA sequence for P703DE5
- SEQ ID NO: 226 is the determined cDNA sequence for 9-A11
- 30 SEQ ID NO: 227 is the determined cDNA sequence for 8-C6
- SEQ ID NO: 228 is the determined cDNA sequence for 8-H7
- SEQ ID NO: 229 is the determined cDNA sequence for JPTPN13

- SEQ ID NO: 230 is the determined cDNA sequence for JPTPN14
SEQ ID NO: 231 is the determined cDNA sequence for JPTPN23
SEQ ID NO: 232 is the determined cDNA sequence for JPTPN24
SEQ ID NO: 233 is the determined cDNA sequence for JPTPN25
5 SEQ ID NO: 234 is the determined cDNA sequence for JPTPN30
SEQ ID NO: 235 is the determined cDNA sequence for JPTPN34
SEQ ID NO: 236 is the determined cDNA sequence for PTPN35
SEQ ID NO: 237 is the determined cDNA sequence for JPTPN36
SEQ ID NO: 238 is the determined cDNA sequence for JPTPN38
10 SEQ ID NO: 239 is the determined cDNA sequence for JPTPN39
SEQ ID NO: 240 is the determined cDNA sequence for JPTPN40
SEQ ID NO: 241 is the determined cDNA sequence for JPTPN41
SEQ ID NO: 242 is the determined cDNA sequence for JPTPN42
SEQ ID NO: 243 is the determined cDNA sequence for JPTPN45
15 SEQ ID NO: 244 is the determined cDNA sequence for JPTPN46
SEQ ID NO: 245 is the determined cDNA sequence for JPTPN51
SEQ ID NO: 246 is the determined cDNA sequence for JPTPN56
SEQ ID NO: 247 is the determined cDNA sequence for PTPN64
SEQ ID NO: 248 is the determined cDNA sequence for JPTPN65
20 SEQ ID NO: 249 is the determined cDNA sequence for JPTPN67
SEQ ID NO: 250 is the determined cDNA sequence for JPTPN76
SEQ ID NO: 251 is the determined cDNA sequence for JPTPN84
SEQ ID NO: 252 is the determined cDNA sequence for JPTPN85
SEQ ID NO: 253 is the determined cDNA sequence for JPTPN86
25 SEQ ID NO: 254 is the determined cDNA sequence for JPTPN87
SEQ ID NO: 255 is the determined cDNA sequence for JPTPN88
SEQ ID NO: 256 is the determined cDNA sequence for JP1F1
SEQ ID NO: 257 is the determined cDNA sequence for JP1F2
SEQ ID NO: 258 is the determined cDNA sequence for JP1C2
30 SEQ ID NO: 259 is the determined cDNA sequence for JP1B1
SEQ ID NO: 260 is the determined cDNA sequence for JP1B2
SEQ ID NO: 261 is the determined cDNA sequence for JP1D3

- SEQ ID NO: 262 is the determined cDNA sequence for JP1A4
SEQ ID NO: 263 is the determined cDNA sequence for JP1F5
SEQ ID NO: 264 is the determined cDNA sequence for JP1E6
SEQ ID NO: 265 is the determined cDNA sequence for JP1D6
5 SEQ ID NO: 266 is the determined cDNA sequence for JP1B5
SEQ ID NO: 267 is the determined cDNA sequence for JP1A6
SEQ ID NO: 268 is the determined cDNA sequence for JP1E8
SEQ ID NO: 269 is the determined cDNA sequence for JP1D7
SEQ ID NO: 270 is the determined cDNA sequence for JP1D9
10 SEQ ID NO: 271 is the determined cDNA sequence for JP1C10
SEQ ID NO: 272 is the determined cDNA sequence for JP1A9
SEQ ID NO: 273 is the determined cDNA sequence for JP1F12
SEQ ID NO: 274 is the determined cDNA sequence for JP1E12
SEQ ID NO: 275 is the determined cDNA sequence for JP1D11
15 SEQ ID NO: 276 is the determined cDNA sequence for JP1C11
SEQ ID NO: 277 is the determined cDNA sequence for JP1C12
SEQ ID NO: 278 is the determined cDNA sequence for JP1B12
SEQ ID NO: 279 is the determined cDNA sequence for JP1A12
SEQ ID NO: 280 is the determined cDNA sequence for JP8G2
20 SEQ ID NO: 281 is the determined cDNA sequence for JP8H1
SEQ ID NO: 282 is the determined cDNA sequence for JP8H2
SEQ ID NO: 283 is the determined cDNA sequence for JP8A3
SEQ ID NO: 284 is the determined cDNA sequence for JP8A4
SEQ ID NO: 285 is the determined cDNA sequence for JP8C3
25 SEQ ID NO: 286 is the determined cDNA sequence for JP8G4
SEQ ID NO: 287 is the determined cDNA sequence for JP8B6
SEQ ID NO: 288 is the determined cDNA sequence for JP8D6
SEQ ID NO: 289 is the determined cDNA sequence for JP8F5
SEQ ID NO: 290 is the determined cDNA sequence for JP8A8
30 SEQ ID NO: 291 is the determined cDNA sequence for JP8C7
SEQ ID NO: 292 is the determined cDNA sequence for JP8D7
SEQ ID NO: 293 is the determined cDNA sequence for P8D8

- SEQ ID NO: 294 is the determined cDNA sequence for JP8E7
SEQ ID NO: 295 is the determined cDNA sequence for JP8F8
SEQ ID NO: 296 is the determined cDNA sequence for JP8G8
SEQ ID NO: 297 is the determined cDNA sequence for JP8B10
5 SEQ ID NO: 298 is the determined cDNA sequence for JP8C10
SEQ ID NO: 299 is the determined cDNA sequence for JP8E9
SEQ ID NO: 300 is the determined cDNA sequence for JP8E10
SEQ ID NO: 301 is the determined cDNA sequence for JP8F9
SEQ ID NO: 302 is the determined cDNA sequence for JP8H9
10 SEQ ID NO: 303 is the determined cDNA sequence for JP8C12
SEQ ID NO: 304 is the determined cDNA sequence for JP8E11
SEQ ID NO: 305 is the determined cDNA sequence for JP8E12
SEQ ID NO: 306 is the amino acid sequence for the peptide PS2#12
SEQ ID NO: 307 is the determined cDNA sequence for P711P
15 SEQ ID NO: 308 is the determined cDNA sequence for P712P
SEQ ID NO: 309 is the determined cDNA sequence for CLONE23
SEQ ID NO: 310 is the determined cDNA sequence for P774P
SEQ ID NO: 311 is the determined cDNA sequence for P775P
SEQ ID NO: 312 is the determined cDNA sequence for P715P
20 SEQ ID NO: 313 is the determined cDNA sequence for P710P
SEQ ID NO: 314 is the determined cDNA sequence for P767P
SEQ ID NO: 315 is the determined cDNA sequence for P768P
SEQ ID NO: 316-325 are the determined cDNA sequences of previously isolated genes
SEQ ID NO: 326 is the determined cDNA sequence for P703PDE5
25 SEQ ID NO: 327 is the predicted amino acid sequence for P703PDE5
SEQ ID NO: 328 is the determined cDNA sequence for P703P6.26
SEQ ID NO: 329 is the predicted amino acid sequence for P703P6.26
SEQ ID NO: 330 is the determined cDNA sequence for P703PX-23
SEQ ID NO: 331 is the predicted amino acid sequence for P703PX-23
30 SEQ ID NO: 332 is the determined full length cDNA sequence for P509S
SEQ ID NO: 333 is the determined extended cDNA sequence for P707P (also referred to as 11-C9)
SEQ ID NO: 334 is the determined cDNA sequence for P714P

- SEQ ID NO: 335 is the determined cDNA sequence for P705P (also referred to as 9-F3)
- SEQ ID NO: 336 is the predicted amino acid sequence for P705P
- SEQ ID NO: 337 is the amino acid sequence of the peptide P1S#10
- SEQ ID NO: 338 is the amino acid sequence of the peptide p5
- 5 SEQ ID NO: 339 is the predicted amino acid sequence of P509S
- SEQ ID NO: 340 is the determined cDNA sequence for P778P
- SEQ ID NO: 341 is the determined cDNA sequence for P786P
- SEQ ID NO: 342 is the determined cDNA sequence for P789P
- SEQ ID NO: 343 is the determined cDNA sequence for a clone showing homology to Homo
- 10 sapiens MM46 mRNA
- SEQ ID NO: 344 is the determined cDNA sequence for a clone showing homology to Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA
- SEQ ID NO: 345 is the determined cDNA sequence for a clone showing homology to Homo sapiens mRNA for E-cadherin
- 15 SEQ ID NO: 346 is the determined cDNA sequence for a clone showing homology to Human nuclear-encoded mitochondrial serine hydroxymethyltransferase (SHMT)
- SEQ ID NO: 347 is the determined cDNA sequence for a clone showing homology to Homo sapiens natural resistance-associated macrophage protein2 (NRAMP2)
- SEQ ID NO: 348 is the determined cDNA sequence for a clone showing homology to Homo
- 20 sapiens phosphoglucomutase-related protein (PGMRP)
- SEQ ID NO: 349 is the determined cDNA sequence for a clone showing homology to Human mRNA for proteasome subunit p40
- SEQ ID NO: 350 is the determined cDNA sequence for P777P
- SEQ ID NO: 351 is the determined cDNA sequence for P779P
- 25 SEQ ID NO: 352 is the determined cDNA sequence for P790P
- SEQ ID NO: 353 is the determined cDNA sequence for P784P
- SEQ ID NO: 354 is the determined cDNA sequence for P776P
- SEQ ID NO: 355 is the determined cDNA sequence for P780P
- SEQ ID NO: 356 is the determined cDNA sequence for P544S
- 30 SEQ ID NO: 357 is the determined cDNA sequence for P745S
- SEQ ID NO: 358 is the determined cDNA sequence for P782P
- SEQ ID NO: 359 is the determined cDNA sequence for P783P

- SEQ ID NO: 360 is the determined cDNA sequence for unknown 17984
- SEQ ID NO: 361 is the determined cDNA sequence for P787P
- SEQ ID NO: 362 is the determined cDNA sequence for P788P
- SEQ ID NO: 363 is the determined cDNA sequence for unknown 17994
- 5 SEQ ID NO: 364 is the determined cDNA sequence for P781P
- SEQ ID NO: 365 is the determined cDNA sequence for P785P
- SEQ ID NO: 366-375 are the determined cDNA sequences for splice variants of B305D.
- SEQ ID NO: 376 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 366.
- 10 SEQ ID NO: 377 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 372.
- SEQ ID NO: 378 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 373.
- SEQ ID NO: 379 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 374.
- 15 SEQ ID NO: 380 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 375.
- SEQ ID NO: 381 is the determined cDNA sequence for B716P.
- SEQ ID NO: 382 is the determined full-length cDNA sequence for P711P.
- 20 SEQ ID NO: 383 is the predicted amino acid sequence for P711P.
- SEQ ID NO: 384 is the cDNA sequence for P1000C.
- SEQ ID NO: 385 is the cDNA sequence for CGI-82.
- SEQ ID NO: 386 is the cDNA sequence for 23320.
- SEQ ID NO: 387 is the cDNA sequence for CGI-69.
- 25 SEQ ID NO: 388 is the cDNA sequence for L-iditol-2-dehydrogenase.
- SEQ ID NO: 389 is the cDNA sequence for 23379.
- SEQ ID NO: 390 is the cDNA sequence for 23381.
- SEQ ID NO: 391 is the cDNA sequence for KIAA0122.
- SEQ ID NO: 392 is the cDNA sequence for 23399.
- 30 SEQ ID NO: 393 is the cDNA sequence for a previously identified gene.
- SEQ ID NO: 394 is the cDNA sequence for HCLBP.
- SEQ ID NO: 395 is the cDNA sequence for transglutaminase.

SEQ ID NO:396 is the cDNA sequence for a previously identified gene.

SEQ ID NO:397 is the cDNA sequence for PAP.

SEQ ID NO:398 is the cDNA sequence for Ets transcription factor PDEF.

SEQ ID NO:399 is the cDNA sequence for hTGR.

5 SEQ ID NO:400 is the cDNA sequence for KIAA0295.

SEQ ID NO:401 is the cDNA sequence for 22545.

SEQ ID NO:402 is the cDNA sequence for 22547.

SEQ ID NO:403 is the cDNA sequence for 22548.

SEQ ID NO:404 is the cDNA sequence for 22550.

10 SEQ ID NO:405 is the cDNA sequence for 22551.

SEQ ID NO:406 is the cDNA sequence for 22552.

SEQ ID NO:407 is the cDNA sequence for 22553.

SEQ ID NO:408 is the cDNA sequence for 22558.

SEQ ID NO:409 is the cDNA sequence for 22562.

15 SEQ ID NO:410 is the cDNA sequence for 22565.

SEQ ID NO:411 is the cDNA sequence for 22567.

SEQ ID NO:412 is the cDNA sequence for 22568.

SEQ ID NO:413 is the cDNA sequence for 22570.

SEQ ID NO:414 is the cDNA sequence for 22571.

20 SEQ ID NO:415 is the cDNA sequence for 22572.

SEQ ID NO:416 is the cDNA sequence for 22573.

SEQ ID NO:417 is the cDNA sequence for 22573.

SEQ ID NO:418 is the cDNA sequence for 22575.

SEQ ID NO:419 is the cDNA sequence for 22580.

25 SEQ ID NO:420 is the cDNA sequence for 22581.

SEQ ID NO:421 is the cDNA sequence for 22582.

SEQ ID NO:422 is the cDNA sequence for 22583.

SEQ ID NO:423 is the cDNA sequence for 22584.

SEQ ID NO:424 is the cDNA sequence for 22585.

30 SEQ ID NO:425 is the cDNA sequence for 22586.

SEQ ID NO:426 is the cDNA sequence for 22587.

SEQ ID NO:427 is the cDNA sequence for 22588.

- SEQ ID NO:428 is the cDNA sequence for 22589.
SEQ ID NO:429 is the cDNA sequence for 22590.
SEQ ID NO:430 is the cDNA sequence for 22591.
SEQ ID NO:431 is the cDNA sequence for 22592.
5 SEQ ID NO:432 is the cDNA sequence for 22593.
SEQ ID NO:433 is the cDNA sequence for 22594.
SEQ ID NO:434 is the cDNA sequence for 22595.
SEQ ID NO:435 is the cDNA sequence for 22596.
SEQ ID NO:436 is the cDNA sequence for 22847.
10 SEQ ID NO:437 is the cDNA sequence for 22848.
SEQ ID NO:438 is the cDNA sequence for 22849.
SEQ ID NO:439 is the cDNA sequence for 22851.
SEQ ID NO:440 is the cDNA sequence for 22852.
SEQ ID NO:441 is the cDNA sequence for 22853.
15 SEQ ID NO:442 is the cDNA sequence for 22854.
SEQ ID NO:443 is the cDNA sequence for 22855.
SEQ ID NO:444 is the cDNA sequence for 22856.
SEQ ID NO:445 is the cDNA sequence for 22857.
SEQ ID NO:446 is the cDNA sequence for 23601.
20 SEQ ID NO:447 is the cDNA sequence for 23602.
SEQ ID NO:448 is the cDNA sequence for 23605.
SEQ ID NO:449 is the cDNA sequence for 23606.
SEQ ID NO:450 is the cDNA sequence for 23612.
SEQ ID NO:451 is the cDNA sequence for 23614.
25 SEQ ID NO:452 is the cDNA sequence for 23618.
SEQ ID NO:453 is the cDNA sequence for 23622.
SEQ ID NO:454 is the cDNA sequence for folate hydrolase.
SEQ ID NO:455 is the cDNA sequence for LIM protein.
SEQ ID NO:456 is the cDNA sequence for a known gene.
30 SEQ ID NO:457 is the cDNA sequence for a known gene.
SEQ ID NO:458 is the cDNA sequence for a previously identified gene.
SEQ ID NO:459 is the cDNA sequence for 23045.

SEQ ID NO:460 is the cDNA sequence for 23032.

SEQ ID NO:461 is the cDNA sequence for 23054.

SEQ ID NO:462-467 are cDNA sequences for known genes.

SEQ ID NO:468-471 are cDNA sequences for P710P.

- 5 SEQ ID NO:472 is a cDNA sequence for P1001C.

SEQ ID NO: 473 is the determined cDNA sequence for a first splice variant of P775P (referred to as 27505).

SEQ ID NO: 474 is the determined cDNA sequence for a second splice variant of P775P (referred to as 19947).

- 10 SEQ ID NO: 475 is the determined cDNA sequence for a third splice variant of P775P (referred to as 19941).

SEQ ID NO: 476 is the determined cDNA sequence for a fourth splice variant of P775P (referred to as 19937).

SEQ ID NO: 477 is a first predicted amino acid sequence encoded by the sequence of SEQ ID NO:

- 15 474.

SEQ ID NO: 478 is a second predicted amino acid sequence encoded by the sequence of SEQ ID NO: 474.

SEQ ID NO: 479 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 475.

- 20 SEQ ID NO: 480 is a first predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 481 is a second predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 482 is a third predicted amino acid sequence encoded by the sequence of SEQ ID NO:

- 25 473.

SEQ ID NO: 483 is a fourth predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 484 is the first 30 amino acids of the *M. tuberculosis* antigen Ra12.

SEQ ID NO: 485 is the PCR primer AW025.

- 30 SEQ ID NO: 486 is the PCR primer AW003.

SEQ ID NO: 487 is the PCR primer AW027.

SEQ ID NO: 488 is the PCR primer AW026.

SEQ ID NO: 489-501 are peptides employed in epitope mapping studies.

SEQ ID NO: 502 is the determined cDNA sequence of the complementarity determining region for the anti-P503S monoclonal antibody 20D4.

5 SEQ ID NO: 503 is the determined cDNA sequence of the complementarity determining region for the anti-P503S monoclonal antibody JA1.

SEQ ID NO: 504 & 505 are peptides employed in epitope mapping studies.

SEQ ID NO: 506 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 8H2.

10 SEQ ID NO: 507 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 7H8.

SEQ ID NO: 508 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 2D4.

SEQ ID NO: 509-522 are peptides employed in epitope mapping studies.

15 SEQ ID NO: 523 is a mature form of P703P used to raise antibodies against P703P. SEQ ID NO: 524 is the putative full-length cDNA sequence of P703P.

SEQ ID NO: 525 is the predicted amino acid sequence encoded by SEQ ID NO: 524.

SEQ ID NO: 526 is the full-length cDNA sequence for P790P.

SEQ ID NO: 527 is the predicted amino acid sequence for P790P.

SEQ ID NO: 528 & 529 are PCR primers.

20 SEQ ID NO: 530 is the cDNA sequence of a splice variant of SEQ ID NO: 366.

SEQ ID NO: 531 is the cDNA sequence of the open reading frame of SEQ ID NO: 530.

SEQ ID NO: 532 is the predicted amino acid encoded by the sequence of SEQ ID NO: 531.

SEQ ID NO: 533 is the DNA sequence of a putative ORF of P775P.

SEQ ID NO: 534 is the predicted amino acid sequence encoded by SEQ ID NO: 533.

25 SEQ ID NO: 535 is a first full-length cDNA sequence for P510S.

SEQ ID NO: 536 is a second full-length cDNA sequence for P510S.

SEQ ID NO: 537 is the predicted amino acid sequence encoded by SEQ ID NO: 535.

SEQ ID NO: 538 is the predicted amino acid sequence encoded by SEQ ID NO: 536.

SEQ ID NO: 539 is the peptide P501S-370.

30 SEQ ID NO: 540 is the peptide P501S-376.

SEQ ID NO: 541-550 are epitopes of P501S.

SEQ ID NO: 551 corresponds to amino acids 543-553 of P501S.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer. The compositions described herein may include prostate-specific polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies, antigen presenting cells (APCs) and/or immune system cells (*e.g.*, T cells). Polypeptides of the present invention generally comprise at least a portion (such as an immunogenic portion) of a prostate-specific protein or a variant thereof. A "prostate-specific protein" is a protein that is expressed in normal prostate and/or prostate tumor cells at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in a non-prostate normal tissue, as determined using a representative assay provided herein. Certain prostate-specific proteins are proteins that react detectably (within an immunoassay, such as an ELISA or Western blot) with antisera of a patient afflicted with prostate cancer. Polynucleotides of the subject invention generally comprise a DNA or RNA sequence that encodes all or a portion of such a polypeptide, or that is complementary to such a sequence. Antibodies are generally immune system proteins, or antigen-binding fragments thereof, that are capable of binding to a polypeptide as described above. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B-cells that express a polypeptide as described above. T cells that may be employed within such compositions are generally T cells that are specific for a polypeptide as described above.

The present invention is based on the discovery of human prostate-specific proteins. Sequences of polynucleotides encoding certain prostate-specific proteins, or portions thereof, are provided in SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382, 384-476, 524, 526, 530, 531, 533, 535 and 536. Sequences of polypeptides comprising at least a portion of a prostate-specific protein are provided in SEQ ID NOs:112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534 and 537-550.

PROSTATE-SPECIFIC PROTEIN POLYNUCLEOTIDES

Any polynucleotide that encodes a prostate-specific protein or a portion or other variant thereof as described herein is encompassed by the present invention. Preferred

polynucleotides comprise at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides and more preferably at least 45 consecutive nucleotides, that encode a portion of a prostate-specific protein. More preferably, a polynucleotide encodes an immunogenic portion of a prostate-specific protein. Polynucleotides complementary to any such sequences are also
5 encompassed by the present invention. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the
10 present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a prostate-specific protein or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions
15 and/or insertions such that the immunogenicity of the encoded polypeptide is not diminished, relative to a native protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native prostate-specific protein or a portion thereof. The
20 term “variants” also encompasses homologous genes of xenogenic origin.

Two polynucleotide or polypeptide sequences are said to be “identical” if the sequence of nucleotides or amino acids in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local
25 regions of sequence similarity. A “comparison window” as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the
30 Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices

for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA* 80:726-730.

Preferably, the “percentage of sequence identity” is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native prostate-specific protein (or a complementary sequence). Suitable moderately stringent conditions include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such

as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Polynucleotides may be prepared using any of a variety of techniques. For example,
5 a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least five fold greater in a prostate-specific than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997).
10 Alternatively, polypeptides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as prostate-specific cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

15 An amplified portion may be used to isolate a full length gene from a suitable library (*e.g.*, a prostate-specific cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes.
20 Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (*e.g.*, by nick-translation or end-labeling with ³²P) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (*see* Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989).
25 Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The
30 complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into

a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments; using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length DNA sequences may also be obtained by analysis of genomic fragments.

Certain nucleic acid sequences of cDNA molecules encoding at least a portion of a prostate-specific protein are provided in SEQ ID NO:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382, 384-476, 524, 526, 530, 531, 533, 535 and 536.

Isolation of these polynucleotides is described below. Each of these prostate-specific proteins was overexpressed in prostate tumor tissue.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis.

5 Modifications in a polynucleotide sequence may also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (*see* Adelman et al., *DNA* 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding a prostate-specific protein, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain
10 portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated *in vivo* (*e.g.*, by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a prostate-specific polypeptide, and administering the transfected cells to the patient).

15 A portion of a sequence complementary to a coding sequence (*i.e.*, an antisense polynucleotide) may also be used as a probe or to modulate gene expression. cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells of tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of a protein. Antisense technology can be used to control gene expression
20 through triple-helix formation, which compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (*see* Gee et al., *In* Huber and Carr, *Molecular and Immunologic Approaches*, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (*e.g.*, promoter, enhancer or transcription initiation site), and block transcription of
25 the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

A portion of a coding sequence, or of a complementary sequence, may also be designed as a probe or primer to detect gene expression. Probes may be labeled with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and still more preferably at least 30
30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3'

ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl-, methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

5 Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector
10 will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

Within certain embodiments, polynucleotides may be formulated so as to permit entry into a cell of a mammal, and expression therein. Such formulations are particularly useful for
15 therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a polynucleotide in a target cell, and any suitable method may be employed. For example, a polynucleotide may be incorporated into a viral vector such as, but not limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (e.g., avian pox virus). The polynucleotides may also be administered as naked plasmid vectors.
20 Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary
25 skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.*, an artificial membrane
30 vesicle). The preparation and use of such systems is well known in the art.

PROSTATE-SPECIFIC POLYPEPTIDES

Within the context of the present invention, polypeptides may comprise at least an immunogenic portion of a prostate-specific protein or a variant thereof, as described herein. As noted above, a "prostate-specific protein" is a protein that is expressed by normal prostate and/or prostate tumor cells. Proteins that are prostate-specific proteins also react detectably within an immunoassay (such as an ELISA) with antisera from a patient with prostate cancer. Polypeptides as described herein may be of any length. Additional sequences derived from the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

An "immunogenic portion," as used herein is a portion of a protein that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of a prostate-specific protein or a variant thereof. Certain preferred immunogenic portions include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other preferred immunogenic portions may contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well known techniques. An immunogenic portion of a native prostate-specific protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the

immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A.

As noted above, a composition may comprise a variant of a native prostate-specific protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native prostate-specific protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially diminished. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein. Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity (determined as described above) to the identified polypeptides.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino

acids that have minimal influence on the immunogenicity, secondary structure and hydrophobic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, higher eukaryotic and plant cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known prostate-specific protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner),

preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

Fusion proteins may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused protein, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are

located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see, for example, Stoute et al. New Engl. J. Med.*, 336:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its

original environment. For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector
5 that is not a part of the natural environment.

BINDING AGENTS

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a prostate-specific protein. As used herein, an
10 antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a prostate-specific protein if it reacts at a detectable level (within, for example, an ELISA) with a prostate-specific protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability to bind may be evaluated by, for example, determining a binding
15 constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known in the art.

20 Binding agents may be further capable of differentiating between patients with and without a cancer, such as prostate cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a prostate-specific protein will generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals
25 without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (*e.g.*, blood, sera, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the
30 above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Most preferably, antibodies employed in the inventive methods have the ability to induce lysis of tumor cells by activation of complement and mediation of antibody-dependent cellular cytotoxicity (ADCC). Antibodies of different classes and subclasses differ in these properties. For example, mouse antibodies of the IgG2a and IgG3 classes are capable of activating serum complement upon binding to target cells which express the antigen against which the antibodies were raised, and can mediate ADCC.

Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells

and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are
5 selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse.
10 Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

The preparation of mouse and rabbit monoclonal antibodies that specifically bind to
15 polypeptides of the present invention is described in detail below. However, the antibodies of the present invention are not limited to those derived from mice. Human antibodies may also be employed in the inventive methods and may prove to be preferable. Such antibodies can be obtained using human hybridomas as described by Cote *et al.* (Monoclonal Antibodies and Cancer Therapy, Alan R. Lisa, p. 77, 1985). The present invention also encompasses antibodies made by
20 recombinant means such as chimeric antibodies, wherein the variable region and constant region are derived from different species, and CDR-grafted antibodies, wherein the complementarity determining region is derived from a different species, as described in US Patents 4,816,567 and 5,225,539. Chimeric antibodies may be prepared by splicing genes for a mouse antibody molecule having a desired antigen specificity together with genes for a human antibody molecule having the
25 desired biological activity, such as activation of human complement and mediation of ADCC (Morrison *et al. Proc. Natl. Acad. Sci. USA* 81:6851, 1984; Neuberger *et al. Nature* 312:604, 1984; Takeda *et al. Nature* 314:452, 1985).

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard
30 techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, *Antibodies: A Laboratory Manual*,

Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to

Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

5 It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or
10 linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

 A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent
15 No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating
20 compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

 A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of
25 a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

T CELLS

30 Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for a prostate-specific protein. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral

blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the ISOLEX™ system, available from Nexell Therapeutics Inc., Irvine, CA (see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated
5 humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a prostate-specific polypeptide, polynucleotide encoding a prostate-specific polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide. Preferably, a prostate-specific
10 polypeptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a prostate-specific polypeptide if the T cells specifically proliferate, secrete cytokines or kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a
15 variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell
20 proliferation can be detected by measuring an increased rate of DNA synthesis (e.g., by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a prostate-specific polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of
25 the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (e.g., TNF or IFN-γ) is indicative of T cell activation (see Coligan et al., *Current Protocols in Immunology*, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a prostate-specific polypeptide, polynucleotide or polypeptide-expressing APC may be CD4⁺ and/or CD8⁺. Prostate-specific protein-specific T cells may be expanded using
30 standard techniques. Within preferred embodiments, the T cells are derived from either a patient or a related, or unrelated, donor and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4⁺ or CD8⁺ T cells that proliferate in response to a prostate-specific polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a prostate-specific polypeptide, or a short peptide
5 corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a prostate-specific polypeptide. Alternatively, one or more T cells that proliferate in the presence of a prostate-specific protein can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

10

PHARMACEUTICAL COMPOSITIONS AND VACCINES

Within certain aspects, polypeptides, polynucleotides, T cells and/or binding agents disclosed herein may be incorporated into pharmaceutical compositions or immunogenic compositions (*i.e.*, vaccines). Pharmaceutical compositions comprise one or more such compounds
15 and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and an immunostimulant. An immunostimulant may be any substance that enhances an immune response to an exogenous antigen. Examples of immunostimulants include adjuvants, biodegradable microspheres (*e.g.*, polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally
20 described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the
25 composition or vaccine.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression
30 systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression

in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.*, polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (*e.g.*, neutral buffered saline or phosphate buffered saline), carbohydrates (*e.g.*, glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA

or glutathione, adjuvants (e.g., aluminum hydroxide) and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of immunostimulants may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- γ , TNF α , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Ribi ImmunoChem Research Inc. (Hamilton, MT; see US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555. Another preferred adjuvant is a saponin, preferably QS21, which may be used alone or in combination with other adjuvants. For example,

an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprises an oil-in-water emulsion and tocopherol. A particularly potent
5 adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210. Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immune response enhancer and a suitable carrier or excipient.

The compositions described herein may be administered as part of a sustained release
10 formulation (*i.e.*, a formulation such as a capsule, sponge or gel (composed of polysaccharides for example) that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix
15 and/or contained within a reservoir surrounded by a rate controlling membrane. Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical
20 compositions and vaccines to facilitate production of an antigen-specific immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the
25 antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or
30 progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy,

Ann. Rev. Med. 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take-up, process and present antigens with high efficiency, and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface
5 receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (see Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone
10 marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into
15 dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this
20 nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II
25 MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide encoding a prostate-specific protein (or portion or other variant thereof) such that the prostate-specific polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place
30 *in vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection

that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells
5 with the prostate-specific polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of
10 the polypeptide.

CANCER THERAPY

In further aspects of the present invention, the compositions described herein may be used for immunotherapy of cancer, such as prostate cancer. Within such methods, pharmaceutical
15 compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. A cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor.
20 Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react
25 against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides disclosed herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not
30 necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer

cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate
5 antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in*
10 *vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte,
15 fibroblast or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies
20 have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see*, for example, Cheever et al., *Immunological Reviews* 157:177, 1997).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back
25 into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions disclosed herein, as well as dosage, will vary from individual to individual, and may be readily established
30 using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered

over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50%
5 above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-
10 vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 25 µg to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active
15 compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a prostate-specific protein generally correlate with an improved clinical outcome. Such immune responses may generally be
20 evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

METHODS FOR DETECTING CANCER

In general, a cancer may be detected in a patient based on the presence of one or
25 more prostate-specific proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as prostate cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the
30 agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer.

In general, a prostate tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. *See, e.g., Harlow and Lane, 5 Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized
10 on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G,
15 protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full
20 length prostate-specific proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or
25 disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization"
30 refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a

membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of
5 binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the
10 binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may
15 be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The
20 amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween
25 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer.
30 Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by

assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains
5 a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of
10 time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group
15 (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a
20 signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is
25 determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest
30 to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along

the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use prostate-specific polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such prostate-specific protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a prostate-specific protein in a biological sample. Within certain methods, a biological sample comprising CD4⁺ and/or CD8⁺ T cells isolated from a patient is incubated with a prostate-specific polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that

expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may
5 be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with prostate-specific polypeptide (*e.g.*, 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of prostate-specific polypeptide to serve as a control. For CD4⁺ T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8⁺ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater
10 and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a prostate-specific protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to
15 amplify a portion of a prostate-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the prostate-specific protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a prostate-specific protein may be used in a hybridization
20 assay to detect the presence of polynucleotide encoding the protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a prostate-specific protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in
25 length. Preferably, oligonucleotide primers and/or probes will hybridize to a polynucleotide encoding a polypeptide disclosed herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15
30 contiguous nucleotides, of a DNA molecule having a sequence recited in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382, 384-476, 524, 526, 530, 531, 533, 535 and 536. Techniques for both PCR based assays and hybridization assays

are well known in the art (*see, for example, Mullis et al., Cold Spring Harbor Symp. Quant. Biol., 51:263, 1987; Erlich ed., PCR Technology, Stockton Press, NY, 1989*).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue,
5 and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or
10 greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the disclosed compositions may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or
15 polynucleotide evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

20 Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

25 As noted above, to improve sensitivity, multiple prostate-specific protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or
30 alternatively, assays for proteins provided herein may be combined with assays for other known tumor antigens.

DIAGNOSTIC KITS

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For
5 example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a prostate-specific protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or
10 indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding a prostate-specific protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a prostate-specific protein. Such an oligonucleotide may be used, for example, within a PCR or
15 hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a prostate-specific protein.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

5 ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC POLYPEPTIDES

This Example describes the isolation of certain prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate
10 tumor poly A⁺ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning
kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol.
Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and
total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the
manufacturer. The poly A⁺ RNA was then purified using a Qiagen oligotex spin column mRNA
15 purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-
strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was
synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with
NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA), the
cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into
20 ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was
prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by
determining the number of independent colonies, the percentage of clones that carried insert, the
average insert size and by sequence analysis. The prostate tumor library contained 1.64×10^7
25 independent colonies, with 70% of clones having an insert and the average insert size being 1745
base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69%
of clones having inserts and the average insert size being 1120 base pairs. For both libraries,
sequence analysis showed that the majority of clones had a full length cDNA sequence and were
synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

30 cDNA library subtraction was performed using the above prostate tumor and normal
pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some
modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as

follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H₂O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As
5 recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H₂O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with
10 BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H₂O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and
15 incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H₂O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA
20 was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (referred to as "prostate subtraction 1").

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and
25 grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively,
30 with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA

library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show
5 some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid
10 sequences are provided in SEQ ID NOS: 112-114. L1-12 is also referred to as P501S.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (referred to as "prostate subtraction 2"). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided
15 in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (referred to as "prostate subtraction spike 2") was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating
20 sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in
25 SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated
30

clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 5 190, respectively.

Additional studies with prostate subtraction spike 2 resulted in the isolation of three more clones. Their sequences were determined as described above and compared to the most recent GenBank. All three clones were found to have homology to known genes, which are Cysteine-rich protein, KIAA0242, and KIAA0280 (SEQ ID NO: 317, 319, and 320, respectively). Further 10 analysis of these clones by Synteni microarray (Synteni, Palo Alto, CA) demonstrated that all three clones were over-expressed in most prostate tumors and prostate BPH, as well as in the majority of normal prostate tissues tested, but low expression in all other normal tissues.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (referred to as "prostate subtraction 3"). This led to the 15 identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 20 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA⁺ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-25 4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

30 cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni,

Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

Additional studies led to the isolation of the full-length cDNA sequence for P509S. This sequence is provided in SEQ ID NO: 332, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 339. Two variant full-length cDNA sequences for P510S are provided in SEQ ID NO: 535 and 536, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 537 and 538, respectively.

EXAMPLE 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE-SPECIFIC POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate-specific polypeptides F1-16, H1-1, J1-17 (also referred to as P502S), L1-12 (also referred to as P501S), F1-12 (also referred to as P504S) and N1-1862 (also referred to as P503S) were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 μ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β -actin levels were determined for each

reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 (P502S) and L1-12 (P501S) appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 (P503S) was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17 (P502S), N1-1862 (P503S) and L1-12 (P501S) are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 (P504S) is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 (P501S) is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 (P502S) was detected in two prostate tumors and not in the other tissues tested. N1-1862 (P503S) was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney,

but not in other tissues tested. F1-12 (P504S) was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The microarray technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following
5 normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 (P501S) was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 (P504S) were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues
10 tested. N1-1862 (P503S) was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in
15 normal spinal cord, and to be undetectable in all other tissues tested.

Further microarray analysis to specifically address the extent to which P501S (SEQ ID NO: 110) was expressed in breast tumor revealed moderate over-expression not only in breast tumor, but also in metastatic breast tumor (2/31), with negligible to low expression in normal tissues. This data suggests that P501S may be over-expressed in various breast tumors as well as in
20 prostate tumors.

The expression levels of 32 ESTs (expressed sequence tags) described by Vasmatzis *et al.* (*Proc. Natl. Acad. Sci. USA* 95:300-304, 1998) in a variety of tumor and normal tissues were examined by microarray technology as described above. Two of these clones (referred to as P1000C and P1001C) were found to be over-expressed in prostate tumor and normal prostate, and
25 expressed at low to undetectable levels in all other tissues tested (normal aorta, thymus, resting and activated PBMC, epithelial cells, spinal cord, adrenal gland, fetal tissues, skin, salivary gland, large intestine, bone marrow, liver, lung, dendritic cells, stomach, lymph nodes, brain, heart, small intestine, skeletal muscle, colon and kidney. The determined cDNA sequences for P1000C and P1001C are provided in SEQ ID NO: 384 and 472, respectively. The sequence of P1001C was
30 found to show some homology to the previously isolated Human mRNA for JM27 protein. No significant homologies were found to the sequence of P1000C.

The expression of the polypeptide encoded by the full length cDNA sequence for F1-12 (also referred to as P504S; SEQ ID NO: 108) was investigated by immunohistochemical analysis. Rabbit-anti-P504S polyclonal antibodies were generated against the full length P504S protein by standard techniques. Subsequent isolation and characterization of the polyclonal antibodies were also performed by techniques well known in the art. Immunohistochemical analysis showed that the P504S polypeptide was expressed in 100% of prostate carcinoma samples tested (n=5).

The rabbit-anti-P504S polyclonal antibody did not appear to label benign prostate cells with the same cytoplasmic granular staining, but rather with light nuclear staining. Analysis of normal tissues revealed that the encoded polypeptide was found to be expressed in some, but not all normal human tissues. Positive cytoplasmic staining with rabbit-anti-P504S polyclonal antibody was found in normal human kidney, liver, brain, colon and lung-associated macrophages, whereas heart and bone marrow were negative.

This data indicates that the P504S polypeptide is present in prostate cancer tissues, and that there are qualitative and quantitative differences in the staining between benign prostatic hyperplasia tissues and prostate cancer tissues, suggesting that this polypeptide may be detected selectively in prostate tumors and therefore be useful in the diagnosis of prostate cancer.

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EXAMPLE 3

ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences
5 for these clones are provided in SEQ ID NO: 41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO: 46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the
10 isolation of more than 180 additional clones, of which 23 clones were found to show no significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-
15 170) were found to have some degree of homology to known genes. Larger cDNA clones containing the P20 sequence represent splice variants of a gene referred to as P703P. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The determined cDNA
20 sequence for an extended spliced form of P703 is provided in SEQ ID NO: 225. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary
25 (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCR as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20, a
30 portion of the P703P gene, was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of

2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, 9-f12 and 9-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, 9-f12 and 9-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequence of 9-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and 9-f12 were found to show some homology to previously identified genes. Further characterization of 7-G6 and 8-G3 showed identity to the known genes PAP and PSA, respectively.

mRNA expression levels for these clones were determined using the micro-array technology described above. The clones 7-G6, 8-G3, 8-B5, 8-B6, 8-D4, 8-D9, 9-F3, 9-F12, 9-H3, 10-A2, 10-A4, 11-C9 and 11-F2 were found to be over-expressed in prostate tumor and normal prostate, with expression in other tissues tested being low or undetectable. Increased expression of 8-F11 was seen in prostate tumor and normal prostate, bladder, skeletal muscle and colon. Increased expression of 10-H10 was seen in prostate tumor and normal prostate, bladder, lung, colon, brain and large intestine. Increased expression of 9-B1 was seen in prostate tumor, breast tumor, and normal prostate, salivary gland, large intestine and skin, with increased expression of 11-C8 being seen in prostate tumor, and normal prostate and large intestine.

An additional cDNA fragment derived from the PCR-based normal prostate subtraction, described above, was found to be prostate specific by both micro-array technology and RT-PCR. The determined cDNA sequence of this clone (referred to as 9-A11) is provided in SEQ ID NO: 226. Comparison of this sequence with those in the public databases revealed 99% identity to the known gene HOXB13.

Further studies led to the isolation of the clones 8-C6 and 8-H7. The determined cDNA sequences for these clones are provided in SEQ ID NO: 227 and 228, respectively. These sequences were found to show some homology to previously isolated ESTs.

PCR and hybridization-based methodologies were employed to obtain longer cDNA sequences for clone P20 (also referred to as P703P), yielding three additional cDNA fragments that progressively extend the 5' end of the gene. These fragments, referred to as P703PDE5, P703P6.26, and P703PX-23 (SEQ ID NO: 326, 328 and 330, with the predicted corresponding amino acid sequences being provided in SEQ ID NO: 327, 329 and 331, respectively) contain additional 5' sequence. P703PDE5 was recovered by screening of a cDNA library (#141-26) with a portion of P703P as a probe. P703P6.26 was recovered from a mixture of three prostate tumor cDNAs and P703PX_23 was recovered from cDNA library (#438-48). Together, the additional sequences include all of the putative mature serine protease along with part of the putative signal sequence. The putative full-length cDNA sequence for P703P is provided in SEQ ID NO: 524, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 525.

Further studies using a PCR-based subtraction library of a prostate tumor pool subtracted against a pool of normal tissues (referred to as JP: PCR subtraction) resulted in the isolation of thirteen additional clones, seven of which did not share any significant homology to known GenBank sequences. The determined cDNA sequences for these seven clones (P711P, P712P, novel 23, P774P, P775P, P710P and P768P) are provided in SEQ ID NO: 307-311, 313 and 315, respectively. The remaining six clones (SEQ ID NO: 316 and 321-325) were shown to share some homology to known genes. By microarray analysis, all thirteen clones showed three or more fold over-expression in prostate tissues, including prostate tumors, BPH and normal prostate as compared to normal non-prostate tissues. Clones P711P, P712P, novel 23 and P768P showed over-expression in most prostate tumors and BPH tissues tested (n=29), and in the majority of normal prostate tissues (n=4), but background to low expression levels in all normal tissues. Clones P774P, P775P and P710P showed comparatively lower expression and expression in fewer prostate tumors and BPH samples, with negative to low expression in normal prostate.

The full-length cDNA for P711P was obtained by employing the partial sequence of SEQ ID NO: 307 to screen a prostate cDNA library. Specifically, a directionally cloned prostate cDNA library was prepared using standard techniques. One million colonies of this library were plated onto LB/Amp plates. Nylon membrane filters were used to lift these colonies, and the cDNAs which were picked up by these filters were denatured and cross-linked to the filters by UV light. The P711P cDNA fragment of SEQ ID NO: 307 was radio-labeled and used to hybridize with these filters. Positive clones were selected, and cDNAs were prepared and sequenced using an automatic Perkin Elmer/Applied Biosystems sequencer. The determined full-length sequence of P711P is provided in SEQ ID NO: 382, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 383.

Using PCR and hybridization-based methodologies, additional cDNA sequence information was derived for two clones described above, 11-C9 and 9-F3, herein after referred to as P707P and P714P, respectively (SEQ ID NO: 333 and 334). After comparison with the most recent GenBank, P707P was found to be a splice variant of the known gene HoxB13. In contrast, no significant homologies to P714P were found.

Clones 8-B3, P89, P98, P130 and P201 (as disclosed in U.S. Patent Application No. 09/020,956, filed February 9, 1998) were found to be contained within one contiguous sequence, referred to as P705P (SEQ ID NO: 335, with the predicted amino acid sequence provided in SEQ ID NO: 336), which was determined to be a splice variant of the known gene NKX 3.1.

Further studies on P775P resulted in the isolation of four additional sequences (SEQ ID NO: 473-476) which are all splice variants of the P775P gene. The sequence of SEQ ID NO: 474 was found to contain two open reading frames (ORFs). The predicted amino acid sequences encoded by these ORFs are provided in SEQ ID NO: 477 and 478. The cDNA sequence of SEQ ID NO: 475 was found to contain an ORF which encodes the amino acid sequence of SEQ ID NO: 479. The cDNA sequence of SEQ ID NO: 473 was found to contain four ORFs. The predicted amino acid sequences encoded by these ORFs are provided in SEQ ID NO: 480-483.

Subsequent studies led to the identification of a genomic region on chromosome 22q11.2, known as the Cat Eye Syndrome region, that contains the five prostate genes P704P, P712P, P774P, P775P and B305D. The relative location of each of these five genes within the genomic region is shown in Fig. 10. This region may therefore be associated with malignant tumors, and other potential tumor genes may be contained within this region. These studies also led

to the identification of a potential open reading frame (ORF) for P775P (provided in SEQ ID NO: 533), which encodes the amino acid sequence of SEQ ID NO: 534.

EXAMPLE 4

SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

EXAMPLE 5

FURTHER ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA library generated from prostate primary tumor mRNA as described above was subtracted with cDNA from normal prostate. The subtraction was performed using a PCR-based protocol (Clontech), which was modified to generate larger fragments. Within this protocol, tester and driver double stranded cDNA were separately digested with five restriction enzymes that recognize six-nucleotide restriction sites (MluI, MscI, PvuII, SalI and StuI). This digestion resulted in an average cDNA size of 600 bp, rather than the average size of 300 bp that results from digestion with RsaI according to the Clontech protocol. This modification did not affect the

subtraction efficiency. Two tester populations were then created with different adapters, and the driver library remained without adapters.

The tester and driver libraries were then hybridized using excess driver cDNA. In the first hybridization step, driver was separately hybridized with each of the two tester cDNA populations. This resulted in populations of (a) unhybridized tester cDNAs, (b) tester cDNAs hybridized to other tester cDNAs, (c) tester cDNAs hybridized to driver cDNAs and (d) unhybridized driver cDNAs. The two separate hybridization reactions were then combined, and rehybridized in the presence of additional denatured driver cDNA. Following this second hybridization, in addition to populations (a) through (d), a fifth population (e) was generated in which tester cDNA with one adapter hybridized to tester cDNA with the second adapter. Accordingly, the second hybridization step resulted in enrichment of differentially expressed sequences which could be used as templates for PCR amplification with adaptor-specific primers.

The ends were then filled in, and PCR amplification was performed using adaptor-specific primers. Only population (e), which contained tester cDNA that did not hybridize to driver cDNA, was amplified exponentially. A second PCR amplification step was then performed, to reduce background and further enrich differentially expressed sequences.

This PCR-based subtraction technique normalizes differentially expressed cDNAs so that rare transcripts that are overexpressed in prostate tumor tissue may be recoverable. Such transcripts would be difficult to recover by traditional subtraction methods.

In addition to genes known to be overexpressed in prostate tumor, seventy-seven further clones were identified. Sequences of these partial cDNAs are provided in SEQ ID NO: 29 to 305. Most of these clones had no significant homology to database sequences. Exceptions were JPTPN23 (SEQ ID NO: 231; similarity to pig valosin-containing protein), JPTPN30 (SEQ ID NO: 234; similarity to rat mRNA for proteasome subunit), JPTPN45 (SEQ ID NO: 243; similarity to rat *norvegicus* cytosolic NADP-dependent isocitrate dehydrogenase), JPTPN46 (SEQ ID NO: 244; similarity to human subclone H8 4 d4 DNA sequence), JP1D6 (SEQ ID NO: 265; similarity to *G. gallus* dynein light chain-A), JP8D6 (SEQ ID NO: 288; similarity to human BAC clone RG016J04), JP8F5 (SEQ ID NO: 289; similarity to human subclone H8 3 b5 DNA sequence), and JP8E9 (SEQ ID NO: 299; similarity to human Alu sequence).

Additional studies using the PCR-based subtraction library consisting of a prostate tumor pool subtracted against a normal prostate pool (referred to as PT-PN PCR subtraction) yielded three additional clones. Comparison of the cDNA sequences of these clones with the most

recent release of GenBank revealed no significant homologies to the two clones referred to as P715P and P767P (SEQ ID NO: 312 and 314). The remaining clone was found to show some homology to the known gene KIAA0056 (SEQ ID NO: 318). Using microarray analysis to measure mRNA expression levels in various tissues, all three clones were found to be over-expressed in prostate tumors and BPH tissues. Specifically, clone P715P was over-expressed in most prostate tumors and BPH tissues by a factor of three or greater, with elevated expression seen in the majority of normal prostate samples and in fetal tissue, but negative to low expression in all other normal tissues. Clone P767P was over-expressed in several prostate tumors and BPH tissues, with moderate expression levels in half of the normal prostate samples, and background to low expression in all other normal tissues tested.

Further analysis, by microarray as described above, of the PT-PN PCR subtraction library and of a DNA subtraction library containing cDNA from prostate tumor subtracted with a pool of normal tissue cDNAs, led to the isolation of 27 additional clones (SEQ ID NO: 340-365 and 381) which were determined to be over-expressed in prostate tumor. The clones of SEQ ID NO: 341, 342, 345, 347, 348, 349, 351, 355-359, 361, 362 and 364 were also found to be expressed in normal prostate. Expression of all 26 clones in a variety of normal tissues was found to be low or undetectable, with the exception of P544S (SEQ ID NO: 356) which was found to be expressed in small intestine. Of the 26 clones, 10 (SEQ ID NO: 340-349) were found to show some homology to previously identified sequences. No significant homologies were found to the clones of SEQ ID NO: 350, 351 and 353-365.

Further studies on the clone of SEQ ID NO: 352 (referred to as P790P) led to the isolation of the full-length cDNA sequence of SEQ ID NO: 526. The corresponding predicted amino acid is provided in SEQ ID NO: 527. Data from two quantitative PCR experiments indicated that P790P is over-expressed in 11/15 tested prostate tumor samples and is expressed at low levels in spinal cord, with no expression being seen in all other normal samples tested. Data from further PCR experiments and microarray experiments showed over-expression in normal prostate and prostate tumor with little or no expression in other tissues tested. P790P was subsequently found to show significant homology to a previously identified G-protein coupled prostate tissue receptor.

EXAMPLE 6

PEPTIDE PRIMING OF MICE AND PROPAGATION OF CTL LINES

5 6.1. This Example illustrates the preparation of a CTL cell line specific for cells expressing the P502S gene.

 Mice expressing the transgene for human HLA A2Kb (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with P2S#12 peptide (VLGWVAEL; SEQ ID NO: 306), which is derived from the P502S gene (also referred to herein as J1-17, SEQ ID
10 NO: 8), as described by Theobald et al., *Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995 with the following modifications. Mice were immunized with 100 μ g of P2S#12 and 120 μ g of an I-A^b binding peptide derived from hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and using a nylon mesh single cell suspensions prepared. Cells were then resuspended at 6×10^6 cells/ml in complete media (RPMI-1640; Gibco
15 BRL, Gaithersburg, MD) containing 10% FCS, 2mM Glutamine (Gibco BRL), sodium pyruvate (Gibco BRL), non-essential amino acids (Gibco BRL), 2×10^{-5} M 2-mercaptoethanol, 50U/ml penicillin and streptomycin, and cultured in the presence of irradiated (3000 rads) P2S#12-pulsed (5mg/ml P2S#12 and 10mg/ml β 2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7 μ g/ml dextran sulfate and 25 μ g/ml LPS for 3 days). Six days later, cells ($5 \times$
20 10^5 /ml) were restimulated with 2.5×10^6 /ml peptide pulsed irradiated (20,000 rads) EL4A2Kb cells (Sherman et al, *Science* 258:815-818, 1992) and 3×10^6 /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20U/ml IL-2. Cells continued to be restimulated on a weekly basis as described, in preparation for cloning the line.

 P2S#12 line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb
25 tumor cells (1×10^4 cells/ well) as stimulators and A2 transgenic spleen cells as feeders (5×10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, clones that were growing were isolated and maintained in culture. Several of these clones demonstrated significantly higher reactivity (lysis) against human fibroblasts (HLA A2Kb expressing) transduced with P502S than against control fibroblasts. An example is presented in
30 Figure 1.

 This data indicates that P2S #12 represents a naturally processed epitope of the P502S protein that is expressed in the context of the human HLA A2Kb molecule.

6.2. This Example illustrates the preparation of murine CTL lines and CTL clones specific for cells expressing the P501S gene.

This series of experiments were performed similarly to that described above. Mice
5 were immunized with the P1S#10 peptide (SEQ ID NO: 337), which is derived from the P501S
gene (also referred to herein as L1-12, SEQ ID NO: 110). The P1S#10 peptide was derived by
analysis of the predicted polypeptide sequence for P501S for potential HLA-A2 binding sequences
as defined by published HLA-A2 binding motifs (Parker, KC, *et al*, *J. Immunol.*, 152:163, 1994).
P1S#10 peptide was synthesized as described in Example 4, and empirically tested for HLA-A2
10 binding using a T cell based competition assay. Predicted A2 binding peptides were tested for their
ability to compete HLA-A2 specific peptide presentation to an HLA-A2 restricted CTL clone
(D150M58), which is specific for the HLA-A2 binding influenza matrix peptide fluM58. D150M58
CTL secretes TNF in response to self-presentation of peptide fluM58. In the competition assay, test
peptides at 100-200 µg/ml were added to cultures of D150M58 CTL in order to bind HLA-A2 on
15 the CTL. After thirty minutes, CTL cultured with test peptides, or control peptides, were tested for
their antigen dose response to the fluM58 peptide in a standard TNF bioassay. As shown in Figure
3, peptide P1S#10 competes HLA-A2 restricted presentation of fluM58, demonstrating that peptide
P1S#10 binds HLA-A2.

Mice expressing the transgene for human HLA A2Kb were immunized as described
20 by Theobald et al. (*Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995) with the following
modifications. Mice were immunized with 62.5µg of P1S #10 and 120µg of an I-A^b binding
peptide derived from Hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three
weeks later these mice were sacrificed and single cell suspensions prepared using a nylon mesh.
Cells were then resuspended at 6×10^6 cells/ml in complete media (as described above) and cultured
25 in the presence of irradiated (3000 rads) P1S#10-pulsed (2µg/ml P1S#10 and 10mg/ml β2-
microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7µg/ml dextran
sulfate and 25µg/ml LPS for 3 days). Six days later cells (5×10^5 /ml) were restimulated with $2.5 \times$
 10^6 /ml peptide-pulsed irradiated (20,000 rads) EL4A2Kb cells, as described above, and 3×10^6 /ml
A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20 U/ml IL-2. Cells were
30 restimulated on a weekly basis in preparation for cloning. After three rounds of *in vitro*
stimulations, one line was generated that recognized P1S#10-pulsed Jurkat A2Kb targets and
P501S-transduced Jurkat targets as shown in Figure 4.

A P1S#10-specific CTL line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells (1×10^4 cells/ well) as stimulators and A2 transgenic spleen cells as feeders (5×10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, viable clones were isolated and maintained in culture. As shown
5 in Figure 5, five of these clones demonstrated specific cytolytic reactivity against P501S-transduced Jurkat A2Kb targets. This data indicates that P1S#10 represents a naturally processed epitope of the P501S protein that is expressed in the context of the human HLA-A2.1 molecule.

EXAMPLE 7

10 PRIMING OF CTL *IN VIVO* USING NAKED DNA IMMUNIZATION WITH A PROSTATE ANTIGEN

The prostate-specific antigen LI-12, as described above, is also referred to as P501S. HLA A2Kb Tg mice (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with 100 μ g P501S in the vector VR1012 either intramuscularly or intradermally.
15 The mice were immunized three times, with a two week interval between immunizations. Two weeks after the last immunization, immune spleen cells were cultured with Jurkat A2Kb-P501S transduced stimulator cells. CTL lines were stimulated weekly. After two weeks of *in vitro* stimulation, CTL activity was assessed against P501S transduced targets. Two out of 8 mice developed strong anti-P501S CTL responses. These results demonstrate that P501S contains at
20 least one naturally processed HLA-A2-restricted CTL epitope.

EXAMPLE 8

25 ABILITY OF HUMAN T CELLS TO RECOGNIZE PROSTATE-SPECIFIC POLYPEPTIDES

This Example illustrates the ability of T cells specific for a prostate tumor polypeptide to recognize human tumor.

Human CD8⁺ T cells were primed *in vitro* to the P2S-12 peptide (SEQ ID NO: 306) derived from P502S (also referred to as J1-17) using dendritic cells according to the protocol of Van
30 Tsai et al. (*Critical Reviews in Immunology* 18:65-75, 1998). The resulting CD8⁺ T cell microcultures were tested for their ability to recognize the P2S-12 peptide presented by autologous fibroblasts or fibroblasts which were transduced to express the P502S gene in a γ -interferon

ELISPOT assay (*see* Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). Briefly, titrating numbers of T cells were assayed in duplicate on 10^4 fibroblasts in the presence of 3 $\mu\text{g/ml}$ human β_2 -microglobulin and 1 $\mu\text{g/ml}$ P2S-12 peptide or control E75 peptide. In addition, T cells were simultaneously assayed on autologous fibroblasts transduced with the P502S gene or as a control, fibroblasts transduced with HER-2/*neu*. Prior to the assay, the fibroblasts were treated with 10 ng/ml γ -interferon for 48 hours to upregulate class I MHC expression. One of the microcultures (#5) demonstrated strong recognition of both peptide pulsed fibroblasts as well as transduced fibroblasts in a γ -interferon ELISPOT assay. Figure 2A demonstrates that there was a strong increase in the number of γ -interferon spots with increasing numbers of T cells on fibroblasts pulsed with the P2S-12 peptide (solid bars) but not with the control E75 peptide (open bars). This shows the ability of these T cells to specifically recognize the P2S-12 peptide. As shown in Figure 2B, this microculture also demonstrated an increase in the number of γ -interferon spots with increasing numbers of T cells on fibroblasts transduced to express the P502S gene but not the HER-2/*neu* gene. These results provide additional confirmatory evidence that the P2S-12 peptide is a naturally processed epitope of the P502S protein. Furthermore, this also demonstrates that there exists in the human T cell repertoire, high affinity T cells which are capable of recognizing this epitope. These T cells should also be capable of recognizing human tumors which express the P502S gene.

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EXAMPLE 9

ELICITATION OF PROSTATE ANTIGEN-SPECIFIC CTL RESPONSES IN HUMAN BLOOD

This Example illustrates the ability of a prostate-specific antigen to elicit a CTL response in blood of normal humans.

Autologous dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal donors by growth for five days in RPMI medium containing 10% human serum, 50 ng/ml GM-CSF and 30 ng/ml IL-4. Following culture, DC were infected overnight with recombinant P501S-expressing vaccinia virus at an M.O.I. of 5 and matured for 8 hours by the addition of 2 micrograms/ml CD40 ligand. Virus was inactivated by UV irradiation, CD8⁺ cells were isolated by positive selection using magnetic beads, and priming cultures were initiated in 24-well plates. Following five stimulation cycles using autologous fibroblasts retrovirally transduced

to express P501S and CD80, CD8+ lines were identified that specifically produced interferon-gamma when stimulated with autologous P501S-transduced fibroblasts. The P501S-specific activity of cell line 3A-1 could be maintained following additional stimulation cycles on autologous B-LCL transduced with P501S. Line 3A-1 was shown to specifically recognize autologous B-LCL transduced to express P501S, but not EGFP-transduced autologous B-LCL, as measured by cytotoxicity assays (^{51}Cr release) and interferon-gamma production (Interferon-gamma Elispot; *see* above and Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). The results of these assays are presented in Figures 6A and 6B.

EXAMPLE 10

IDENTIFICATION OF A NATURALLY PROCESSED CTL EPITOPE CONTAINED WITHIN A PROSTATE-SPECIFIC ANTIGEN

The 9-mer peptide p5 (SEQ ID NO: 338) was derived from the P703P antigen (also referred to as P20). The p5 peptide is immunogenic in human HLA-A2 donors and is a naturally processed epitope. Antigen specific human CD8+ T cells can be primed following repeated *in vitro* stimulations with monocytes pulsed with p5 peptide. These CTL specifically recognize p5-pulsed and P703P-transduced target cells in both ELISPOT (as described above) and chromium release assays. Additionally, immunization of HLA-A2Kb transgenic mice with p5 leads to the generation of CTL lines which recognize a variety of HLA-A2Kb or HLA-A2 transduced target cells expressing P703P.

Initial studies demonstrating that p5 is a naturally processed epitope were done using HLA-A2Kb transgenic mice. HLA-A2Kb transgenic mice were immunized subcutaneously in the footpad with 100 μg of p5 peptide together with 140 μg of hepatitis B virus core peptide (a Th peptide) in Freund's incomplete adjuvant. Three weeks post immunization, spleen cells from immunized mice were stimulated *in vitro* with peptide-pulsed LPS blasts. CTL activity was assessed by chromium release assay five days after primary *in vitro* stimulation. Retrovirally transduced cells expressing the control antigen P703P and HLA-A2Kb were used as targets. CTL lines that specifically recognized both p5-pulsed targets as well as P703P-expressing targets were identified.

Human *in vitro* priming experiments demonstrated that the p5 peptide is immunogenic in humans. Dendritic cells (DC) were differentiated from monocyte cultures derived

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Using *in vitro* whole-gene priming with P501S-vaccinia infected DC (see, for example, Yee et al, *The Journal of Immunology*, 157(9):4079-86, 1996), human CTL lines were derived that specifically recognize autologous fibroblasts transduced with P501S (also known as L1-12), as determined by interferon- γ ELISPOT analysis as described above. Using a panel of
5 HLA-mismatched B-LCL lines transduced with P501S, these CTL lines were shown to be likely restricted to HLAB class I allele. Specifically, dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by growing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, DC were infected overnight with recombinant P501S vaccinia virus at a
10 multiplicity of infection (M.O.I) of five, and matured overnight by the addition of 3 μ g/ml CD40 ligand. Virus was inactivated by UV irradiation. CD8⁺ T cells were isolated using a magnetic bead system, and priming cultures were initiated using standard culture techniques. Cultures were restimulated every 7-10 days using autologous primary fibroblasts retrovirally transduced with P501S and CD80. Following four stimulation cycles, CD8⁺ T cell lines were identified that
15 specifically produced interferon- γ when stimulated with P501S and CD80-transduced autologous fibroblasts. A panel of HLA-mismatched B-LCL lines transduced with P501S were generated to define the restriction allele of the response. By measuring interferon- γ in an ELISPOT assay, the P501S specific response was shown to be likely restricted by HLA B alleles. These results demonstrate that a CD8⁺ CTL response to P501S can be elicited.

20 To identify the epitope(s) recognized, cDNA encoding P501S was fragmented by various restriction digests, and sub-cloned into the retroviral expression vector pBIB-KS. Retroviral supernatants were generated by transfection of the helper packaging line Phoenix-Ampho. Supernatants were then used to transduce Jurkat/A2Kb cells for CTL screening. CTL were screened in IFN- γ ELISPOT assays against these A2Kb targets transduced with the "library" of P501S
25 fragments. Initial positive fragments P501S/H3 and P501S/F2 were sequenced and found to encode amino acids 106-553 and amino acids 136-547, respectively, of SEQ ID NO: 113. A truncation of H3 was made to encode amino acid residues 106-351 of SEQ ID NO: 113, which was unable to stimulate the CTL, thus localizing the epitope to amino acid residues 351-547. Additional fragments encoding amino acids 1-472 (Fragment A) and amino acids 1-351 (Fragment B) were
30 also constructed. Fragment A but not Fragment B stimulated the CTL thus localizing the epitope to amino acid residues 351-472. Overlapping 20-mer and 18-mer peptides representing this region were tested by pulsing Jurkat/A2Kb cells versus CTL in an IFN- γ assay. Only peptides

P501S-369(20) and P501S-369(18) stimulated the CTL. Nine-mer and 10-mer peptides representing this region were synthesized and similarly tested. Peptide P501S-370 (SEQ ID NO: 539) was the minimal 9-mer giving a strong response. Peptide P501S-376 (SEQ ID NO: 540) also gave a weak response, suggesting that it might represent a cross-reactive epitope.

5 In subsequent studies, the ability of primary human B cells transduced with P501S to prime MHC class I-restricted, P501S-specific, autologous CD8 T cells was examined. Primary B cells were derived from PBMC of a homozygous HLA-A2 donor by culture in CD40 ligand and IL-4, transduced at high frequency with recombinant P501S in the vector pBIB, and selected with blastocidin-S. For *in vitro* priming, purified CD8⁺ T cells were cultured with autologous CD40
10 ligand + IL-4 derived, P501S-transduced B cells in a 96-well microculture format. These CTL microcultures were re-stimulated with P501S-transduced B cells and then assayed for specificity. Following this initial screen, microcultures with significant signal above background were cloned on autologous EBV-transformed B cells (BLCL), also transduced with P501S. Using IFN-gamma ELISPOT for detection, several of these CD8 T cell clones were found to be specific for P501S, as
15 demonstrated by reactivity to BLCL/P501S but not BLCL transduced with control antigen. It was further demonstrated that the anti-P501S CD8 T cell specificity is HLA-A2-restricted. First, antibody blocking experiments with anti-HLA-A,B,C monoclonal antibody (W6.32), anti-HLA-B,C monoclonal antibody (B1.23.2) and a control monoclonal antibody showed that only the anti-HLA-A,B,C antibody blocked recognition of P501S-expressing autologous BLCL. Secondly, the anti-
20 P501S CTL also recognized an HLA-A2 matched, heterologous BLCL transduced with P501S, but not the corresponding EGFP transduced control BLCL.

EXAMPLE 13

IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY MICROARRAY ANALYSIS

25

This Example describes the isolation of certain prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in
30 prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 372 clones were identified, and 319 were successfully sequenced. Table I presents a summary of these clones, which are shown in SEQ ID NOs:385-400. Of these sequences

SEQ ID NOs:386, 389, 390 and 392 correspond to novel genes, and SEQ ID NOs: 393 and 396 correspond to previously identified sequences. The others (SEQ ID NOs:385, 387, 388, 391, 394, 395 and 397-400) correspond to known sequences, as shown in Table I.

5

Table I

Summary of Prostate Tumor Antigens

Known Genes	Previously Identified Genes	Novel Genes
T-cell gamma chain	P504S	23379 (SEQ ID NO:389)
Kallikrein	P1000C	23399 (SEQ ID NO:392)
Vector	P501S	23320 (SEQ ID NO:386)
CGI-82 protein mRNA (23319; SEQ ID NO:385)	P503S	23381 (SEQ ID NO:390)
PSA	P510S	
Ald. 6 Dehyd.	P784P	
L-iditol-2 dehydrogenase (23376; SEQ ID NO:388)	P502S	
Ets transcription factor PDEF (22672; SEQ ID NO:398)	P706P	
hTGR (22678; SEQ ID NO:399)	19142.2, bangur.seq (22621; SEQ ID NO:396)	
KIAA0295(22685; SEQ ID NO:400)	5566.1 Wang (23404; SEQ ID NO:393)	
Prostatic Acid Phosphatase(22655; SEQ ID NO:397)	P712P	
transglutaminase (22611; SEQ ID NO:395)	P778P	
HDLBP (23508; SEQ ID NO:394)		
CGI-69 Protein(23367; SEQ ID NO:387)		
KIAA0122(23383; SEQ ID NO:391)		
TEEG		

CGI-82 showed 4.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 43% of prostate tumors, 25% normal prostate, not detected in other normal tissues tested. L-iditol-2 dehydrogenase showed 4.94 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 90% of prostate tumors, 100% of normal prostate, and not detected in other normal tissues tested. Its transcription factor PDEF showed 5.55 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% prostate tumors, 25% normal prostate and not detected in other normal tissues tested. hTGR1 showed 9.11 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 63% of prostate tumors and is not detected in normal tissues tested including normal prostate. KIAA0295 showed 5.59 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% of prostate tumors, low to undetectable in normal tissues tested including normal prostate tissues. Prostatic acid phosphatase showed 9.14 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 67% of prostate tumors, 50% of normal prostate, and not detected in other normal tissues tested. Transglutaminase showed 14.84 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 30% of prostate tumors, 50% of normal prostate, and is not detected in other normal tissues tested. High density lipoprotein binding protein (HDLBP) showed 28.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% of normal prostate, and is undetectable in all other normal tissues tested. CGI-69 showed 3.56 fold over-expression in prostate tissues as compared to other normal tissues tested. It is a low abundant gene, detected in more than 90% of prostate tumors, and in 75% normal prostate tissues. The expression of this gene in normal tissues was very low. KIAA0122 showed 4.24 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 57% of prostate tumors, it was undetectable in all normal tissues tested including normal prostate tissues. 19142.2 bangur showed 23.25 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors and 100% of normal prostate. It was undetectable in other normal tissues tested. 5566.1 Wang showed 3.31 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% normal prostate and was also over-expressed in normal bone marrow, pancreas, and activated PBMC. Novel clone 23379 showed 4.86 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in 97%

of prostate tumors and 75% normal prostate and is undetectable in all other normal tissues tested. Novel clone 23399 showed 4.09 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 27% of prostate tumors and was undetectable in all normal tissues tested including normal prostate tissues. Novel clone 23320 showed 3.15 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in all prostate tumors and 50% of normal prostate tissues. It was also expressed in normal colon and trachea. Other normal tissues do not express this gene at high level.

EXAMPLE 14

IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY ELECTRONIC SUBTRACTION

This Example describes the use of an electronic subtraction technique to identify prostate-specific antigens.

Potential prostate-specific genes present in the GenBank human EST database were identified by electronic subtraction (similar to that described by Vasmatizis et al., *Proc. Natl. Acad. Sci. USA* 95:300-304, 1998). The sequences of EST clones (43,482) derived from various prostate libraries were obtained from the GenBank public human EST database. Each prostate EST sequence was used as a query sequence in a BLASTN (National Center for Biotechnology Information) search against the human EST database. All matches considered identical (length of matching sequence >100 base pairs, density of identical matches over this region > 70%) were grouped (aligned) together in a cluster. Clusters containing more than 200 ESTs were discarded since they probably represented repetitive elements or highly expressed genes such as those for ribosomal proteins. If two or more clusters shared common ESTs, those clusters were grouped together into a "supercluster," resulting in 4,345 prostate superclusters.

Records for the 479 human cDNA libraries represented in the GenBank release were downloaded to create a database of these cDNA library records. These 479 cDNA libraries were grouped into three groups: Plus (normal prostate and prostate tumor libraries, and breast cell line libraries, in which expression was desired), Minus (libraries from other normal adult tissues, in which expression was not desirable), and Other (libraries from fetal tissue, infant tissue, tissues found only in women, non-prostate tumors and cell lines other than prostate cell lines, in which

expression was considered to be irrelevant). A summary of these library groups is presented in Table II.

Table II

Prostate cDNA Libraries and ESTs

Library	# of Libraries	# of ESTs
Plus	25	43,482
Normal	11	18,875
Tumor	11	21,769
Cell lines	3	2,838
Minus	166	
Other	287	

Each supercluster was analyzed in terms of the ESTs within the supercluster. The tissue source of each EST clone was noted and used to classify the superclusters into four groups:

10 Type 1- EST clones found in the Plus group libraries only; no expression detected in Minus or Other group libraries; Type 2- EST clones derived from the Plus and Other group libraries only; no expression detected in the Minus group; Type 3- EST clones derived from the Plus, Minus and Other group libraries, but the number of ESTs derived from the Plus group is higher than in either the Minus or Other groups; and Type 4- EST clones derived from Plus, Minus and Other group

15 libraries, but the number derived from the Plus group is higher than the number derived from the Minus group. This analysis identified 4,345 breast clusters (*see* Table III). From these clusters, 3,172 EST clones were ordered from Research Genetics, Inc., and were received as frozen glycerol stocks in 96-well plates.

Table III
Prostate Cluster Summary

Type	# of Superclusters	# of ESTs Ordered
1	688	677
2	2899	2484
3	85	11
4	673	0
Total	4345	3172

The EST clone inserts were PCR-amplified using amino-linked PCR primers for Synteni microarray analysis. When more than one PCR product was obtained for a particular clone, that PCR product was not used for expression analysis. In total, 2,528 clones from the electronic subtraction method were analyzed by microarray analysis to identify electronic subtraction breast clones that had high levels of tumor vs. normal tissue mRNA. Such screens were performed using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Within these analyses, the clones were arrayed on the chip, which was then probed with fluorescent probes generated from normal and tumor prostate cDNA, as well as various other normal tissues. The slides were scanned and the fluorescence intensity was measured.

Clones with an expression ratio greater than 3 (*i.e.*, the level in prostate tumor and normal prostate mRNA was at least three times the level in other normal tissue mRNA) were identified as prostate tumor-specific sequences (Table IV). The sequences of these clones are provided in SEQ ID NO: 401-453, with certain novel sequences shown in SEQ ID NO: 407, 413, 416-419, 422, 426, 427 and 450.

Table IV
Prostate-tumor Specific Clones

SEQ ID NO.	Sequence Designation	Comments
401	22545	previously identified P1000C
402	22547	previously identified P704P
403	22548	known
404	22550	known
405	22551	PSA
406	22552	prostate secretory protein 94
407	22553	novel
408	22558	previously identified P509S
409	22562	glandular kallikrein
410	22565	previously identified P1000C
411	22567	PAP
412	22568	B1006C (breast tumor antigen)
413	22570	novel
414	22571	PSA
415	22572	previously identified P706P
416	22573	novel
417	22574	novel
418	22575	novel
419	22580	novel
420	22581	PAP
421	22582	prostatic secretory protein 94
422	22583	novel
423	22584	prostatic secretory protein 94
424	22585	prostatic secretory protein 94
425	22586	known
426	22587	novel
427	22588	novel
428	22589	PAP
429	22590	known
430	22591	PSA
431	22592	known
432	22593	Previously identified P777P
433	22594	T cell receptor gamma chain
434	22595	Previously identified P705P
435	22596	Previously identified P707P
436	22847	PAP
437	22848	known
438	22849	prostatic secretory protein 57
439	22851	PAP

440	22852	PAP
441	22853	PAP
442	22854	previously identified P509S
443	22855	previously identified P705P
444	22856	previously identified P774P
445	22857	PSA
446	23601	previously identified P777P
447	23602	PSA
448	23605	PSA
449	23606	PSA
450	23612	novel
451	23614	PSA
452	23618	previously identified P1000C
453	23622	previously identified P705P

EXAMPLE 15

FURTHER IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY MICROARRAY
ANALYSIS

5

This Example describes the isolation of additional prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened
10 using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 142 clones were identified and sequenced. Certain of these clones are shown in SEQ ID NO: 454-467. Of these sequences, SEQ ID NO: 459-461 represent novel genes. The others (SEQ ID NO: 454-458 and 461-467) correspond to known sequences.

15

EXAMPLE 16

FURTHER CHARACTERIZATION OF PROSTATE-SPECIFIC ANTIGEN P710P

20

This Example describes the full length cloning of P710P.

The prostate cDNA library described above was screened with the P710P fragment described above. One million colonies were plated on LB/Ampicillin plates. Nylon membrane

filters were used to lift these colonies, and the cDNAs picked up by these filters were then denatured and cross-linked to the filters by UV light. The P710P fragment was radiolabeled and used to hybridize with the filters. Positive cDNA clones were selected and their cDNAs recovered and sequenced by an automatic Perkin Elmer/Applied Biosystems Division Sequencer. Four
5 sequences were obtained, and are presented in SEQ ID NO: 468-471. These sequences appear to represent different splice variants of the P710P gene.

EXAMPLE 17

PROTEIN EXPRESSION OF THE PROSTATE-SPECIFIC ANTIGEN P501S

10

This example describes the expression and purification of the prostate-specific antigen P501S in *E. coli*, baculovirus and mammalian cells.

a) Expression in *E. coli*

15 Expression of the full-length form of P501S was attempted by first cloning P501S without the leader sequence (amino acids 36-553 of SEQ ID NO: 113) downstream of the first 30 amino acids of the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 484) in pET17b. Specifically, P501S DNA was used to perform PCR using the primers AW025 (SEQ ID NO: 485) and AW003 (SEQ ID NO: 486). AW025 is a sense cloning primer that contains a HindIII site. AW003 is an
20 antisense cloning primer that contains an EcoRI site. DNA amplification was performed using 5 µl 10X Pfu buffer, 1 µl 20 mM dNTPs, 1 µl each of the PCR primers at 10 µM concentration, 40 µl water, 1 µl Pfu DNA polymerase (Stratagene, La Jolla, CA) and 1 µl DNA at 100 ng/µl. Denaturation at 95°C was performed for 30 sec, followed by 10 cycles of 95°C for 30 sec, 60°C for 1 min and by 72°C for 3 min. 20 cycles of 95°C for 30 sec, 65°C for 1 min and by 72°C for 3 min,
25 and lastly by 1 cycle of 72°C for 10 min. The PCR product was cloned to Ra12m/pET17b using HindIII and EcoRI. The sequence of the resulting fusion construct (referred to as Ra12-P501S-F) was confirmed by DNA sequencing.

The fusion construct was transformed into BL21(DE3)pLysE, pLysS and CodonPlus *E. coli* (Stratagene) and grown overnight in LB broth with kanamycin. The resulting culture was
30 induced with IPTG. Protein was transferred to PVDF membrane and blocked with 5% non-fat milk (in PBS-Tween buffer), washed three times and incubated with mouse anti-His tag antibody (Clontech) for 1 hour. The membrane was washed 3 times and probed with HRP-Protein A

(Zymed) for 30 min. Finally, the membrane was washed 3 times and developed with ECL (Amersham). No expression was detected by Western blot. Similarly, no expression was detected by Western blot when the Ra12-P501S-F fusion was used for expression in BL21CodonPlus by CE6 phage (Invitrogen).

5 An N-terminal fragment of P501S (amino acids 36-325 of SEQ ID NO: 113) was cloned down-stream of the first 30 amino acids of the *M. tuberculosis* antigen Ra12 in pET17b as follows. P501S DNA was used to perform PCR using the primers AW025 (SEQ ID NO: 485) and AW027 (SEQ ID NO: 487). AW027 is an antisense cloning primer that contains an EcoRI site and a stop codon. DNA amplification was performed essentially as described above. The resulting PCR
10 product was cloned to Ra12 in pET17b at the HindIII and EcoRI sites. The fusion construct (referred to as Ra12-P501S-N) was confirmed by DNA sequencing.

The Ra12-P501S-N fusion construct was used for expression in BL21(DE3)pLysE, pLysS and CodonPlus, essentially as described above. Using Western blot analysis, protein bands were observed at the expected molecular weight of 36 kDa. Some high molecular weight bands
15 were also observed, probably due to aggregation of the recombinant protein. No expression was detected by Western blot when the Ra12-P501S-F fusion was used for expression in BL21CodonPlus by CE6 phage.

A fusion construct comprising a C-terminal portion of P501S (amino acids 257-553 of SEQ ID NO: 113) located down-stream of the first 30 amino acids of the *M. tuberculosis* antigen
20 Ra12 (SEQ ID NO: 484) was prepared as follows. P501S DNA was used to perform PCR using the primers AW026 (SEQ ID NO: 488) and AW003 (SEQ ID NO: 486). AW026 is a sense cloning primer that contains a HindIII site. DNA amplification was performed essentially as described above. The resulting PCR product was cloned to Ra12 in pET17b at the HindIII and EcoRI sites. The sequence for the fusion construct (referred to as Ra12-P501S-C) was confirmed.

25 The Ra12-P501S-C fusion construct was used for expression in BL21(DE3)pLysE, pLysS and CodonPlus, as described above. A small amount of protein was detected by Western blot, with some molecular weight aggregates also being observed. Expression was also detected by Western blot when the Ra12-P501S-C fusion was used for expression in BL21CodonPlus induced by CE6 phage.

b) Expression of P501S in Baculovirus

The Bac-to-Bac baculovirus expression system (BRL Life Technologies, Inc.) was used to express P501S protein in insect cells. Full-length P501S (SEQ ID NO: 113) was amplified by PCR and cloned into the XbaI site of the donor plasmid pFastBacI. The recombinant bacmid and baculovirus were prepared according to the manufacturer's instructions. The recombinant baculovirus was amplified in Sf9 cells and the high titer viral stocks were utilized to infect High Five cells (Invitrogen) to make the recombinant protein. The identity of the full-length protein was confirmed by N-terminal sequencing of the recombinant protein and by Western blot analysis (Figure 7). Specifically, 0.6 million High Five cells in 6-well plates were infected with either the unrelated control virus BV/ECD_PD (lane 2), with recombinant baculovirus for P501S at different amounts or MOIs (lanes 4-8), or were uninfected (lane 3). Cell lysates were run on SDS-PAGE under reducing conditions and analyzed by Western blot with the anti-P501S monoclonal antibody P501S-10E3-G4D3 (prepared as described below). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

The localization of recombinant P501S in the insect cells was investigated as follows. The insect cells overexpressing P501S were fractionated into fractions of nucleus, mitochondria, membrane and cytosol. Equal amounts of protein from each fraction were analyzed by Western blot with a monoclonal antibody against P501S. Due to the scheme of fractionation, both nucleus and mitochondria fractions contain some plasma membrane components. However, the membrane fraction is basically free from mitochondria and nucleus. P501S was found to be present in all fractions that contain the membrane component, suggesting that P501S may be associated with plasma membrane of the insect cells expressing the recombinant protein.

c) Expression of P501S in mammalian cells

Full-length P501S (553AA) was cloned into various mammalian expression vectors, including pCEP4 (Invitrogen), pVR1012 (Vical, San Diego, CA) and a modified form of the retroviral vector pBMN, referred to as pBIB. Transfection of P501S/pCEP4 and P501S/pVR1012 into HEK293 fibroblasts was carried out using the Fugene transfection reagent (Boehringer Mannheim). Briefly, 2 ul of Fugene reagent was diluted into 100 ul of serum-free media and incubated at room temperature for 5-10 min. This mixture was added to 1 ug of P501S plasmid DNA, mixed briefly and incubated for 30 minutes at room temperature. The Fugene/DNA mixture

was added to cells and incubated for 24-48 hours. Expression of recombinant P501S in transfected HEK293 fibroblasts was detected by means of Western blot employing a monoclonal antibody to P501S.

Transfection of p501S/pCEP4 into CHO-K cells (American Type Culture Collection, Rockville, MD) was carried out using GenePorter transfection reagent (Gene Therapy Systems, San Diego, CA). Briefly, 15 μ l of GenePorter was diluted in 500 μ l of serum-free media and incubated at room temperature for 10 min. The GenePorter/media mixture was added to 2 μ g of plasmid DNA that was diluted in 500 μ l of serum-free media, mixed briefly and incubated for 30 min at room temperature. CHO-K cells were rinsed in PBS to remove serum proteins, and the GenePorter/DNA mix was added and incubated for 5 hours. The transfected cells were then fed an equal volume of 2x media and incubated for 24-48 hours.

FACS analysis of P501S transiently infected CHO-K cells, demonstrated surface expression of P501S. Expression was detected using rabbit polyclonal antisera raised against a P501S peptide, as described below. Flow cytometric analysis was performed using a FaCScan (Becton Dickinson), and the data were analyzed using the Cell Quest program.

EXAMPLE 18

PREPARATION AND CHARACTERIZATION OF ANTIBODIES AGAINST PROSTATE-SPECIFIC POLYPEPTIDES

20 **a) Preparation and Characterization of Antibodies against P501S**

A murine monoclonal antibody directed against the carboxy-terminus of the prostate-specific antigen P501S was prepared as follows.

A truncated fragment of P501S (amino acids 355-526 of SEQ ID NO: 113) was generated and cloned into the pET28b vector (Novagen) and expressed in *E. coli* as a thioredoxin fusion protein with a histidine tag. The trx-P501S fusion protein was purified by nickel chromatography, digested with thrombin to remove the trx fragment and further purified by an acid precipitation procedure followed by reverse phase HPLC.

Mice were immunized with truncated P501S protein. Serum bleeds from mice that potentially contained anti-P501S polyclonal sera were tested for P501S-specific reactivity using ELISA assays with purified P501S and trx-P501S proteins. Serum bleeds that appeared to react specifically with P501S were then screened for P501S reactivity by Western analysis. Mice that contained a P501S-specific antibody component were sacrificed and spleen cells were used to

generate anti-P501S antibody producing hybridomas using standard techniques. Hybridoma supernatants were tested for P501S-specific reactivity initially by ELISA, and subsequently by FACS analysis of reactivity with P501S transduced cells. Based on these results, a monoclonal hybridoma referred to as 10E3 was chosen for further subcloning. A number of subclones were generated, tested for specific reactivity to P501S using ELISA and typed for IgG isotype. The results of this analysis are shown below in Table V. Of the 16 subclones tested, the monoclonal antibody 10E3-G4-D3 was selected for further study.

Table V

Isotype analysis of murine anti-P501S monoclonal antibodies

Hybridoma clone	Isotype	Estimated [Ig] in supernatant (μg/ml)
4D11	IgG1	14.6
1G1	IgG1	0.6
4F6	IgG1	72
4H5	IgG1	13.8
4H5-E12	IgG1	10.7
4H5-EH2	IgG1	9.2
4H5-H2-A10	IgG1	10
4H5-H2-A3	IgG1	12.8
4H5-H2-A10-G6	IgG1	13.6
4H5-H2-B11	IgG1	12.3
10E3	IgG2a	3.4
10E3-D4	IgG2a	3.8
10E3-D4-G3	IgG2a	9.5
10E3-D4-G6	IgG2a	10.4
10E3-E7	IgG2a	6.5
8H12	IgG2a	0.6

The specificity of 10E3-G4-D3 for P501S was examined by FACS analysis. Specifically, cells were fixed (2% formaldehyde, 10 minutes), permeabilized (0.1% saponin, 10 minutes) and stained with 10E3-G4-D3 at 0.5 – 1 μg/ml, followed by incubation with a secondary, FITC-conjugated goat anti-mouse Ig antibody (Pharmingen, San Diego, CA). Cells were then analyzed for FITC fluorescence using an Excalibur fluorescence activated cell sorter. For FACS analysis of transduced cells, B-LCL were retrovirally transduced with P501S. For analysis of infected cells, B-LCL were infected with a vaccinia vector that expresses P501S. To demonstrate

specificity in these assays, B-LCL transduced with a different antigen (P703P) and uninfected B-LCL vectors were utilized. 10E3-G4-D3 was shown to bind with P501S-transduced B-LCL and also with P501S-infected B-LCL, but not with either uninfected cells or P703P-transduced cells.

To determine whether the epitope recognized by 10E3-G4-D3 was found on the surface or in an intracellular compartment of cells, B-LCL were transduced with P501S or HLA-B8 as a control antigen and either fixed and permeabilized as described above or directly stained with 10E3-G4-D3 and analyzed as above. Specific recognition of P501S by 10E3-G4-D3 was found to require permeabilization, suggesting that the epitope recognized by this antibody is intracellular.

The reactivity of 10E3-G4-D3 with the three prostate tumor cell lines Lncap, PC-3 and DU-145, which are known to express high, medium and very low levels of P501S, respectively, was examined by permeabilizing the cells and treating them as described above. Higher reactivity of 10E3-G4-D3 was seen with Lncap than with PC-3, which in turn showed higher reactivity than DU-145. These results are in agreement with the real time PCR and demonstrate that the antibody specifically recognizes P501S in these tumor cell lines and that the epitope recognized in prostate tumor cell lines is also intracellular.

Specificity of 10E3-G4-D3 for P501S was also demonstrated by Western blot analysis. Lysates from the prostate tumor cell lines Lncap, DU-145 and PC-3, from P501S-transiently transfected HEK293 cells, and from non-transfected HEK293 cells were generated. Western blot analysis of these lysates with 10E3-G4-D3 revealed a 46 kDa immunoreactive band in Lncap, PC-3 and P501S-transfected HEK cells, but not in DU-145 cells or non-transfected HEK293 cells. P501S mRNA expression is consistent with these results since semi-quantitative PCR analysis revealed that P501S mRNA is expressed in Lncap, to a lesser but detectable level in PC-3 and not at all in DU-145 cells. Bacterially expressed and purified recombinant P501S (referred to as P501SStr2) was recognized by 10E3-G4-D3 (24 kDa), as was full-length P501S that was transiently expressed in HEK293 cells using either the expression vector VR1012 or pCEP4. Although the predicted molecular weight of P501S is 60.5 kDa, both transfected and "native" P501S run at a slightly lower mobility due to its hydrophobic nature.

Immunohistochemical analysis was performed on prostate tumor and a panel of normal tissue sections (prostate, adrenal, breast, cervix, colon, duodenum, gall bladder, ileum, kidney, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis). Tissue samples were fixed in formalin solution for 24 hours and embedded in paraffin before being sliced into 10 micron sections. Tissue sections were permeabilized and incubated with 10E3-G4-D3 antibody for 1 hr.

HRP-labeled anti-mouse followed by incubation with DAB chromogen was used to visualize P501S immunoreactivity. P501S was found to be highly expressed in both normal prostate and prostate tumor tissue but was not detected in any of the other tissues tested.

To identify the epitope recognized by 10E3-G4-D3, an epitope mapping approach was pursued. A series of 13 overlapping 20-21 mers (5 amino acid overlap; SEQ ID NO: 489-501) was synthesized that spanned the fragment of P501S used to generate 10E3-G4-D3. Flat bottom 96 well microtiter plates were coated with either the peptides or the P501S fragment used to immunize mice, at 1 microgram/ml for 2 hours at 37 °C. Wells were then aspirated and blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature, and subsequently washed in PBS containing 0.1% Tween 20 (PBST). Purified antibody 10E3-G4-D3 was added at 2 fold dilutions (1000 ng – 16 ng) in PBST and incubated for 30 minutes at room temperature. This was followed by washing 6 times with PBST and subsequently incubating with HRP-conjugated donkey anti-mouse IgG (H+L) Affinipure F(ab') fragment (Jackson Immunoresearch, West Grove, PA) at 1:20000 for 30 minutes. Plates were then washed and incubated for 15 minutes in tetramethyl benzidine. Reactions were stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. As shown in Fig. 8, reactivity was seen with the peptide of SEQ ID NO: 496 (corresponding to amino acids 439-459 of P501S) and with the P501S fragment but not with the remaining peptides, demonstrating that the epitope recognized by 10E3-G4-D3 is localized to amino acids 439-459 of SEQ ID NO: 113.

In order to further evaluate the tissue specificity of P501S, multi-array immunohistochemical analysis was performed on approximately 4700 different human tissues encompassing all the major normal organs as well as neoplasias derived from these tissues. Sixty-five of these human tissue samples were of prostate origin. Tissue sections 0.6 mm in diameter were formalin-fixed and paraffin embedded. Samples were pretreated with HIER using 10 mM citrate buffer pH 6.0 and boiling for 10 min. Sections were stained with 10E3-G4-D3 and P501S immunoreactivity was visualized with HRP. All the 65 prostate tissues samples (5 normal, 55 untreated prostate tumors, 5 hormone refractory prostate tumors) were positive, showing distinct perinuclear staining. All other tissues examined were negative for P501S expression.

b) Preparation and Characterization of Antibodies against P503S

A fragment of P503S (amino acids 113-241 of SEQ ID NO: 114) was expressed and purified from bacteria essentially as described above for P501S and used to immunize both rabbits

and mice. Mouse monoclonal antibodies were isolated using standard hybridoma technology as described above. Rabbit monoclonal antibodies were isolated using Selected Lymphocyte Antibody Method (SLAM) technology at Immgenics Pharmaceuticals (Vancouver, BC, Canada). Table VI, below, lists the monoclonal antibodies that were developed against P503S.

5

Table VI

Antibody	Species
20D4	Rabbit
JA1	Rabbit
1A4	Mouse
1C3	Mouse
1C9	Mouse
1D12	Mouse
2A11	Mouse
2H9	Mouse
4H7	Mouse
8A8	Mouse
8D10	Mouse
9C12	Mouse
6D12	Mouse

The DNA sequences encoding the complementarity determining regions (CDRs) for the rabbit monoclonal antibodies 20D4 and JA1 were determined and are provided in SEQ ID NO: 502 and 503, respectively.

In order to better define the epitope binding region of each of the antibodies, a series of overlapping peptides were generated that span amino acids 109-213 of SEQ ID NO: 114. These peptides were used to epitope map the anti-P503S monoclonal antibodies by ELISA as follows.

The recombinant fragment of P503S that was employed as the immunogen was used as a positive control. Ninety-six well microtiter plates were coated with either peptide or recombinant antigen at 20 ng/well overnight at 4 °C. Plates were aspirated and blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature then washed in PBS containing 0.1% Tween 20 (PBST). Purified rabbit monoclonal antibodies diluted in PBST were added to the wells and incubated for 30 min at room temperature. This was followed by washing 6 times with PBST and incubation with Protein-A HRP conjugate at a 1:2000 dilution for a further 30 min. Plates were washed six times in PBST and incubated with tetramethylbenzidine (TMB) substrate for a further

15 min. The reaction was stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. ELISA with the mouse monoclonal antibodies was performed with supernatants from tissue culture run neat in the assay.

All of the antibodies bound to the recombinant P503S fragment, with the exception
5 of the negative control SP2 supernatant. 20D4, JA1 and 1D12 bound strictly to peptide #2101 (SEQ ID NO: 504), which corresponds to amino acids 151-169 of SEQ ID NO: 114. 1C3 bound to peptide #2102 (SEQ ID NO: 505), which corresponds to amino acids 165-184 of SEQ ID NO: 114. 9C12 bound to peptide #2099 (SEQ ID NO: 522), which corresponds to amino acids 120-139 of SEQ ID NO: 114. The other antibodies bind to regions that were not examined in these studies.

10 Subsequent to epitope mapping, the antibodies were tested by FACS analysis on a cell line that stably expressed P503S to confirm that the antibodies bind to cell surface epitopes. Cells stably transfected with a control plasmid were employed as a negative control. Cells were stained live with no fixative. 0.5 ug of anti-P503S monoclonal antibody was added and cells were incubated on ice for 30 min before being washed twice and incubated with a FITC-labelled goat
15 anti-rabbit or mouse secondary antibody for 20 min. After being washed twice, cells were analyzed with an Excalibur fluorescent activated cell sorter. The monoclonal antibodies 1C3, 1D12, 9C12, 20D4 and JA1, but not 8D3, were found to bind to a cell surface epitope of P503S.

In order to determine which tissues express P503S, immunohistochemical analysis was performed, essentially as described above, on a panel of normal tissues (prostate, adrenal,
20 breast, cervix, colon, duodenum, gall bladder, ileum, kidney, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis). HRP-labeled anti-mouse or anti-rabbit antibody followed by incubation with TMB was used to visualize P503S immunoreactivity. P503S was found to be highly expressed in prostate tissue, with lower levels of expression being observed in cervix, colon, ileum and kidney, and no expression being observed in adrenal, breast, duodenum, gall bladder, ovary,
25 pancreas, parotid gland, skeletal muscle, spleen and testis.

Western blot analysis was used to characterize anti-P503S monoclonal antibody specificity. SDS-PAGE was performed on recombinant (rec) P503S expressed in and purified from bacteria and on lysates from HEK293 cells transfected with full length P503S. Protein was transferred to nitrocellulose and then Western blotted with each of the anti-P503S monoclonal
30 antibodies (20D4, JA1, 1D12, 6D12 and 9C12) at an antibody concentration of 1 ug/ml. Protein was detected using horse radish peroxidase (HRP) conjugated to either a goat anti-mouse monoclonal antibody or to protein A-sepharose. The monoclonal antibody 20D4 detected the

appropriate molecular weight 14 kDa recombinant P503S (amino acids 113-241) and the 23.5 kDa species in the HEK293 cell lysates transfected with full length P503S. Other anti-P503S monoclonal antibodies displayed similar specificity by Western blot.

5 **c) Preparation and Characterization of Antibodies against P703P**

Rabbits were immunized with either a truncated (P703Ptrl; SEQ ID NO: 172) or full-length mature form (P703Pfl; SEQ ID NO: 523) of recombinant P703P protein was expressed in and purified from bacteria as described above. Affinity purified polyclonal antibody was generated using immunogen P703Pfl or P703Ptrl attached to a solid support. Rabbit monoclonal antibodies were isolated using SLAM technology at Immgenics Pharmaceuticals. Table VII below lists both the polyclonal and monoclonal antibodies that were generated against P703P.

Table VII

Antibody	Immunogen	Species/type
Aff. Purif. P703P (truncated); #2594	P703Ptrl	Rabbit polyclonal
Aff. Purif. P703P (full length); #9245	P703Pfl	Rabbit polyclonal
2D4	P703Ptrl	Rabbit monoclonal
8H2	P703Ptrl	Rabbit monoclonal
7H8	P703Ptrl	Rabbit monoclonal

15

The DNA sequences encoding the complementarity determining regions (CDRs) for the rabbit monoclonal antibodies 8H2, 7H8 and 2D4 were determined and are provided in SEQ ID NO: 506-508, respectively.

Epitope mapping studies were performed as described above. Monoclonal antibodies 2D4 and 7H8 were found to specifically bind to the peptides of SEQ ID NO: 509 (corresponding to amino acids 145-159 of SEQ ID NO: 172) and SEQ ID NO: 510 (corresponding to amino acids 11-25 of SEQ ID NO: 172), respectively. The polyclonal antibody 2594 was found to bind to the peptides of SEQ ID NO: 511-514, with the polyclonal antibody 9427 binding to the peptides of SEQ ID NO: 515-517.

The specificity of the anti-P703P antibodies was determined by Western blot analysis as follows. SDS-PAGE was performed on (1) bacterially expressed recombinant antigen; (2) lysates of HEK293 cells and Ltk^{-/-} cells either untransfected or transfected with a plasmid

expressing full length P703P; and (3) supernatant isolated from these cell cultures. Protein was transferred to nitrocellulose and then Western blotted using the anti-P703P polyclonal antibody #2594 at an antibody concentration of 1 ug/ml. Protein was detected using horse radish peroxidase (HRP) conjugated to an anti-rabbit antibody. A 35 kDa immunoreactive band could be observed with recombinant P703P. Recombinant P703P runs at a slightly higher molecular weight since it is epitope tagged. In lysates and supernatants from cells transfected with full length P703P, a 30 kDa band corresponding to P703P was observed. To assure specificity, lysates from HEK293 cells stably transfected with a control plasmid were also tested and were negative for P703P expression. Other anti-P703P antibodies showed similar results.

Immunohistochemical studies were performed as described above, using anti-P703P monoclonal antibody. P703P was found to be expressed at high levels in normal prostate and prostate tumor tissue but was not detectable in all other tissues tested (breast tumor, lung tumor and normal kidney).

EXAMPLE 19

CHARACTERIZATION OF CELL SURFACE EXPRESSION AND CHROMOSOME LOCALIZATION OF THE PROSTATE-SPECIFIC ANTIGEN P501S

This example describes studies demonstrating that the prostate-specific antigen P501S is expressed on the surface of cells, together with studies to determine the probable chromosomal location of P501S.

The protein P501S (SEQ ID NO: 113) is predicted to have 11 transmembrane domains. Based on the discovery that the epitope recognized by the anti-P501S monoclonal antibody 10E3-G4-D3 (described above in Example 17) is intracellular, it was predicted that following transmembrane determinants would allow the prediction of extracellular domains of P501S. Fig. 9 is a schematic representation of the P501S protein showing the predicted location of the transmembrane domains and the intracellular epitope described in Example 17. Underlined sequence represents the predicted transmembrane domains, bold sequence represents the predicted extracellular domains, and italicized sequence represents the predicted intracellular domains. Sequence that is both bold and underlined represents sequence employed to generate polyclonal rabbit serum. The location of the transmembrane domains was predicted using HHMTOP as

described by Tusnady and Simon (Principles Governing Amino Acid Composition of Integral Membrane Proteins: Applications to Topology Prediction, *J. Mol. Biol.* 283:489-506, 1998).

Based on Fig. 9, the P501S domain flanked by the transmembrane domains corresponding to amino acids 274-295 and 323-342 is predicted to be extracellular. The peptide of SEQ ID NO: 518 corresponds to amino acids 306-320 of P501S and lies in the predicted extracellular domain. The peptide of SEQ ID NO: 519, which is identical to the peptide of SEQ ID NO: 518 with the exception of the substitution of the histidine with an asparagine, was synthesized as described above. A Cys-Gly was added to the C-terminus of the peptide to facilitate conjugation to the carrier protein. Cleavage of the peptide from the solid support was carried out using the following cleavage mixture: trifluoroacetic acid:ethanediol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for two hours, the peptide was precipitated in cold ether. The peptide pellet was then dissolved in 10% v/v acetic acid and lyophilized prior to purification by C18 reverse phase hplc. A gradient of 5-60% acetonitrile (containing 0.05% TFA) in water (containing 0.05% TFA) was used to elute the peptide. The purity of the peptide was verified by hplc and mass spectrometry, and was determined to be >95%. The purified peptide was used to generate rabbit polyclonal antisera as described above.

Surface expression of P501S was examined by FACS analysis. Cells were stained with the polyclonal anti-P501S peptide serum at 10 µg/ml, washed, incubated with a secondary FITC-conjugated goat anti-rabbit Ig antibody (ICN), washed and analyzed for FITC fluorescence using an Excalibur fluorescence activated cell sorter. For FACS analysis of transduced cells, B-LCL were retrovirally transduced with P501S. To demonstrate specificity in these assays, B-LCL transduced with an irrelevant antigen (P703P) or nontransduced were stained in parallel. For FACS analysis of prostate tumor cell lines, Lncap, PC-3 and DU-145 were utilized. Prostate tumor cell lines were dissociated from tissue culture plates using cell dissociation medium and stained as above. All samples were treated with propidium iodide (PI) prior to FACS analysis, and data was obtained from PI-excluding (i.e. intact and non-permeabilized) cells. The rabbit polyclonal serum generated against the peptide of SEQ ID NO: 519 was shown to specifically recognize the surface of cells transduced to express P501S, demonstrating that the epitope recognized by the polyclonal serum is extracellular.

To determine biochemically if P501S is expressed on the cell surface, peripheral membranes from Lncap cells were isolated and subjected to Western blot analysis. Specifically, Lncap cells were lysed using a dounce homogenizer in 5 ml of homogenization buffer (250 mM

sucrose, 10 mM HEPES, 1mM EDTA, pH 8.0, 1 complete protease inhibitor tablet (Boehringer Mannheim)). Lysate samples were spun at 1000 g for 5 min at 4 °C. The supernatant was then spun at 8000g for 10 min at 4 °C. Supernatant from the 8000g spin was recovered and subjected to a 100,000g spin for 30 min at 4 °C to recover peripheral membrane. Samples were then separated by SDS-PAGE and Western blotted with the mouse monoclonal antibody 10E3-G4-D3 (described above in Example 17) using conditions described above. Recombinant purified P501S, as well as HEK293 cells transfected with and over-expressing P501S were included as positive controls for P501S detection. LCL cell lysate was included as a negative control. P501S could be detected in Lncap total cell lysate, the 8000g (internal membrane) fraction and also in the 100,000g (plasma membrane) fraction. These results indicate that P501S is expressed at, and localizes to, the peripheral membrane.

To demonstrate that the rabbit polyclonal antiserum generated to the peptide of SEQ ID NO: 519 specifically recognizes this peptide as well as the corresponding native peptide of SEQ ID NO: 518, ELISA analyses were performed. For these analyses, flat-bottomed 96 well microtiter plates were coated with either the peptide of SEQ ID NO: 519, the longer peptide of SEQ ID NO: 520 that spans the entire predicted extracellular domain, the peptide of SEQ ID NO: 521 which represents the epitope recognized by the P501S-specific antibody 10E3-G4-D3, or a P501S fragment (corresponding to amino acids 355-526 of SEQ ID NO: 113) that does not include the immunizing peptide sequence, at 1 µg/ml for 2 hours at 37 °C. Wells were aspirated, blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature and subsequently washed in PBS containing 0.1% Tween 20 (PBST). Purified anti-P501S polyclonal rabbit serum was added at 2 fold dilutions (1000 ng - 125 ng) in PBST and incubated for 30 min at room temperature. This was followed by washing 6 times with PBST and incubating with HRP-conjugated goat anti-rabbit IgG (H+L) Affinipure F(ab') fragment at 1:20000 for 30 min. Plates were then washed and incubated for 15 min in tetramethyl benzidine. Reactions were stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. As shown in Fig. 11, the anti-P501S polyclonal rabbit serum specifically recognized the peptide of SEQ ID NO: 519 used in the immunization as well as the longer peptide of SEQ ID NO: 520, but did not recognize the irrelevant P501S-derived peptides and fragments.

In further studies, rabbits were immunized with peptides derived from the P501S sequence and predicted to be either extracellular or intracellular, as shown in Fig. 9. Polyclonal rabbit sera were isolated and polyclonal antibodies in the serum were purified, as described above.

To determine specific reactivity with P501S, FACS analysis was employed, utilizing either B-LCL transduced with P501S or the irrelevant antigen P703P, of B-LCL infected with vaccinia virus-expressing P501S. For surface expression, dead and non-intact cells were excluded from the analysis as described above. For intracellular staining, cells were fixed and permeabilized as described above. Rabbit polyclonal serum generated against the peptide of SEQ ID NO: 548, which corresponds to amino acids 181-198 of P501S, was found to recognize a surface epitope of P501S. Rabbit polyclonal serum generated against the peptide SEQ ID NO: 551, which corresponds to amino acids 543-553 of P501S, was found to recognize an epitope that was either potentially extracellular or intracellular since in different experiments intact or permeabilized cells were recognized by the polyclonal sera. Based on similar deductive reasoning, the sequences of SEQ ID NO: 541-547, 549 and 550, which correspond to amino acids 109-122, 539-553, 509-520, 37-54, 342-359, 295-323, 217-274, 143-160 and 75-88, respectively, of P501S, can be considered to be potential surface epitopes of P501S recognized by antibodies.

The chromosomal location of P501S was determined using the GeneBridge 4 Radiation Hybrid panel (Research Genetics). The PCR primers of SEQ ID NO: 528 and 529 were employed in PCR with DNA pools from the hybrid panel according to the manufacturer's directions. After 38 cycles of amplification, the reaction products were separated on a 1.2% agarose gel, and the results were analyzed through the Whitehead Institute/MIT Center for Genome Research web server (<http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl>) to determine the probable chromosomal location. Using this approach, P501S was mapped to the long arm of chromosome 1 at WI-9641 between q32 and q42. This region of chromosome 1 has been linked to prostate cancer susceptibility in hereditary prostate cancer (Smith *et al. Science* 274:1371-1374, 1996 and Berthon *et al. Am. J. Hum. Genet.* 62:1416-1424, 1998). These results suggest that P501S may play a role in prostate cancer malignancy.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the present invention is not limited except as by the appended claims.

CLAIMS

1. An isolated polypeptide comprising at least an immunogenic portion of a prostate-specific protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(a) sequences recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536;

(b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and

(c) complements of any of the sequence of (a) or (b).

2. An isolated polypeptide according to claim 1, wherein the polypeptide comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID No: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing polynucleotide sequences.

3. An isolated polypeptide comprising a sequence recited in any one of SEQ ID NO: 108, 112, 113, 114, 172, 176, 178, 327, 329, 331, 339, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534 and 537-550.

4. An isolated polynucleotide encoding at least 15 contiguous amino acid residues of a prostate-specific protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with antigen-specific antisera is not substantially diminished, wherein the protein
5 comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413,
10 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing sequences.

5. An isolated polynucleotide encoding a prostate-specific protein, or a
15 variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396,
20 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing sequences.

6. An isolated polynucleotide comprising a sequence recited in any one
25 of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530,
30 531, 533, 535 and 536.

7. An isolated polynucleotide comprising a sequence that hybridizes under moderately stringent conditions to a sequence recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536.

8. An isolated polynucleotide complementary to a polynucleotide according to any one of claims 4-7.

9. An expression vector comprising a polynucleotide according to any one of claims 4-8.

10. A host cell transformed or transfected with an expression vector according to claim 9.

11. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a prostate-specific protein, the protein comprising an amino acid sequence encoded by a polynucleotide sequence recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536 or a complement of any of the foregoing polynucleotide sequences.

12. A monoclonal antibody that specifically binds to an amino acid sequence selected from the group consisting of SEQ ID NO: 496, 504, 505, 509-517, 519, 520, 522 and 539-551.
- 5 13. A monoclonal antibody comprising a complementarity determining region selected from the group consisting of SEQ ID NO: 502, 503 and 506-508.
14. A fusion protein comprising at least one polypeptide according to
10 claim 1.
15. A fusion protein according to claim 14, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with a polynucleotide encoding the fusion protein.
- 15 16. A fusion protein according to claim 14, wherein the fusion protein comprises a T helper epitope that is not present within the polypeptide of claim 1.
17. A fusion protein according to claim 14, wherein the fusion protein
20 comprises an affinity tag.
18. An isolated polynucleotide encoding a fusion protein according to claim 14.
- 25 19.. A pharmaceutical composition comprising a physiologically acceptable carrier and at least one component selected from the group consisting of:
- (a) a polypeptide according to claim 1;
 - (b) a polynucleotide according to claim 4;
 - (c) an antibody according to any one of claims 11-13;
 - 30 (d) a fusion protein according to claim 14; and

(e) a polynucleotide according to claim 18.

20. A vaccine comprising an immunostimulant and at least one component selected from the group consisting of:

- 5 (a) a polypeptide according to claim 1;
(b) a polynucleotide according to claim 4;
(c) an antibody according to any one of claims 11-13;
(d) a fusion protein according to claim 14; and
(e) a polynucleotide according to claim 18.

10

21. A vaccine according to claim 20, wherein the immunostimulant is an adjuvant.

22. A vaccine according to claim 20, wherein the immunostimulant
15 induces a predominantly Type I response.

23. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a pharmaceutical composition according to claim 19.

20

24. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a vaccine according to claim 20.

25. A pharmaceutical composition comprising an antigen-presenting cell
25 that expresses a polypeptide according to claim 1, in combination with a pharmaceutically acceptable carrier or excipient.

26. A pharmaceutical composition according to claim 25, wherein the antigen presenting cell is a dendritic cell or a macrophage.

27. A vaccine comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with an immunostimulant.

5 28. A vaccine according to claim 27, wherein the immunostimulant is an adjuvant.

29. A vaccine according to claim 27, wherein the immunostimulant induces a predominantly Type I response.

10

30. A vaccine according to claim 27, wherein the antigen-presenting cell is a dendritic cell.

31. A method for inhibiting the development of a cancer in a patient,
15 comprising administering to a patient an effective amount of an antigen-presenting cell that expresses a polypeptide encoded by a polynucleotide recited in any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536, and thereby inhibiting the development of a cancer in the patient.

20

32. A method according to claim 31, wherein the antigen-presenting cell is a dendritic cell.

33. A method according to any one of claims 23, 24 and 31, wherein the
25 cancer is prostate cancer.

34. A method for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a prostate-specific protein, wherein the protein comprises an amino acid sequence that is
30 encoded by a polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536; and

(ii) complements of the foregoing polynucleotides;

5 wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the prostate-specific protein from the sample.

35. A method according to claim 34, wherein the biological sample is
10 blood or a fraction thereof.

36. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated according to the method of claim 50.

15

37. A method for stimulating and/or expanding T cells specific for a prostate-specific protein, comprising contacting T cells with at least one component selected from the group consisting of:

(i) a polypeptide according to claim 1;

20 (ii) a polypeptide encoded by a polynucleotide comprising a sequence provided in any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536;

(iii) a polynucleotide encoding a polypeptide of (i) or (ii); and

(iv) an antigen presenting cell that expresses a polypeptide of (i) or (ii),
25 under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

38. An isolated T cell population, comprising T cells prepared according to the method of claim 37.

30

39. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population according to claim 38.

5 40. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

- (i) a polypeptide according to claim 1;
- 10 (ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536;
- (iii) a polynucleotide encoding a polypeptide of (i) or (ii); or
- 15 (iv) an antigen-presenting cell that expresses a polypeptide of (i) or (ii);

such that T cells proliferate; and

(b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.

20

41. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

- 25 (i) a polypeptide according to claim 1;
- (ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536;
- 30 (iii) a polynucleotide encoding a polypeptide of (i) or (ii); or

(iv) an antigen-presenting cell that expresses a polypeptide of (i) or (ii);

such that T cells proliferate;

(b) cloning at least one proliferated cell to provide cloned T cells; and

5 (c) administering to the patient an effective amount of the cloned T cells, and thereby inhibiting the development of a cancer in the patient.

42. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

10 (a) contacting a biological sample obtained from a patient with a binding agent that binds to a prostate-specific protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NO: 1-111,
15 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536; and

(ii) complements of the foregoing polynucleotides;

(b) detecting in the sample an amount of polypeptide that binds to the binding agent; and

20 (c) comparing the amount of polypeptide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

43. A method according to claim 42, wherein the binding agent is an antibody.

25

44. A method according to claim 43, wherein the antibody is a monoclonal antibody.

45. A method according to claim 42, wherein the cancer is prostate
30 cancer.

46. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

- 5 (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a prostate-specific protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence of any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing polynucleotides;
- 10 (b) detecting in the sample an amount of polypeptide that binds to the binding agent;
- (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and
- (d) comparing the amount of polypeptide detected in step (c) to the
15 amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

47. A method according to claim 46, wherein the binding agent is an antibody.

20

48. A method according to claim 47, wherein the antibody is a monoclonal antibody.

49. A method according to claim 46, wherein the cancer is a prostate
25 cancer.

50. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

- 30 (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate-specific protein,

wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence of any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing polynucleotides;

5 (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(c) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

10

51. A method according to claim 50, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

15

52. A method according to claim 50, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

53. A method for monitoring the progression of a cancer in a patient,
20 comprising the steps of:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate-specific protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence of any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315,
25 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing polynucleotides;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide;

(c) repeating steps (a) and (b) using a biological sample obtained from
30 the patient at a subsequent point in time; and

(d) comparing the amount of polynucleotide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

5 54. A method according to claim 53, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

10 55. A method according to claim 53, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

 56. A diagnostic kit, comprising:
 (a) one or more antibodies according to claim 11; and
15 (b) a detection reagent comprising a reporter group.

 57. A kit according to claim 56, wherein the antibodies are immobilized on a solid support.

20 58. A kit according to claim 56, wherein the detection reagent comprises an anti-immunoglobulin, protein G, protein A or lectin.

 59. A kit according to claim 56, wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups,
25 enzymes, biotin and dye particles.

 60. An oligonucleotide comprising 10 to 40 contiguous nucleotides that hybridize under moderately stringent conditions to a polynucleotide that encodes a prostate-specific protein, wherein the protein comprises an amino acid sequence that is
30 encoded by a polynucleotide sequence recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45,

47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing polynucleotides.

61. A oligonucleotide according to claim 60, wherein the oligonucleotide comprises 10-40 contiguous nucleotides recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-476, 524, 526, 530, 531, 533, 535 and 536.

15

62. A diagnostic kit, comprising:

(a) an oligonucleotide according to claim 61; and

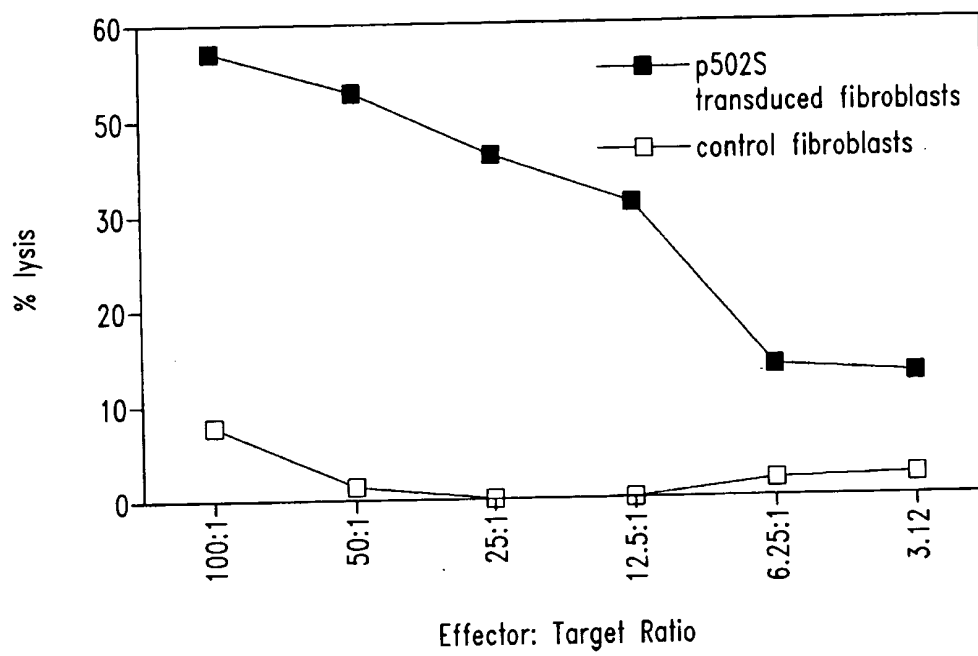
(b) a diagnostic reagent for use in a polymerase chain reaction or hybridization assay.

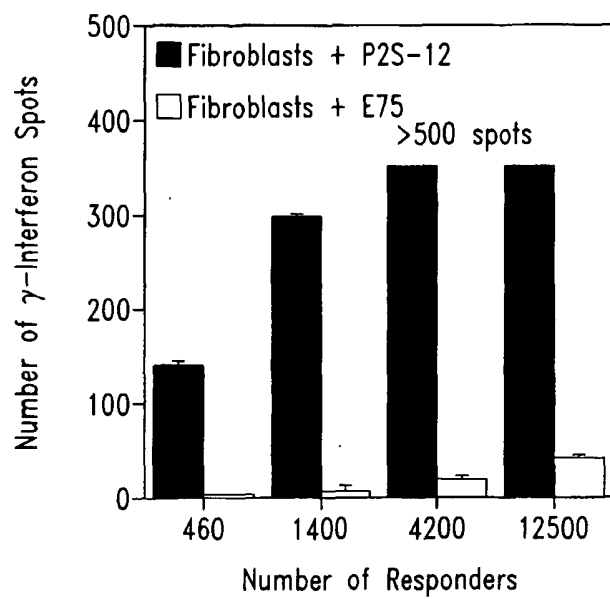
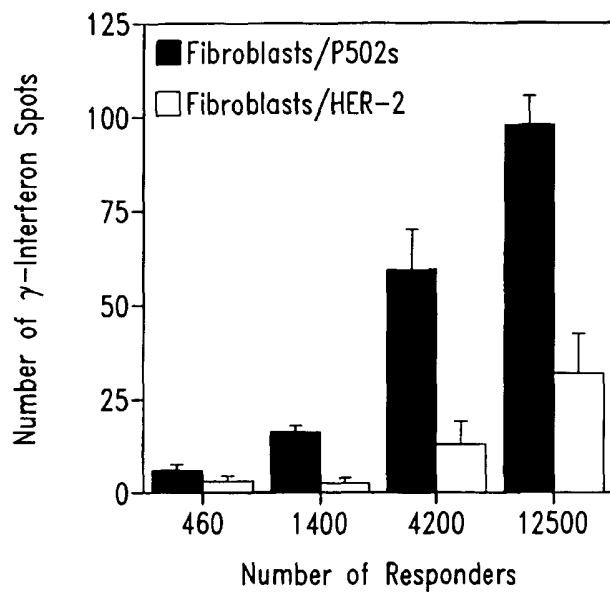
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63. A host cell according to claim 10, wherein the cell is selected from the group consisting of: *E. coli*, baculovirus and mammalian cells.

64. A recombinant protein produced by a host cell according to claim 10.

25

*Fig. 1*

*Fig. 2A**Fig. 2B*

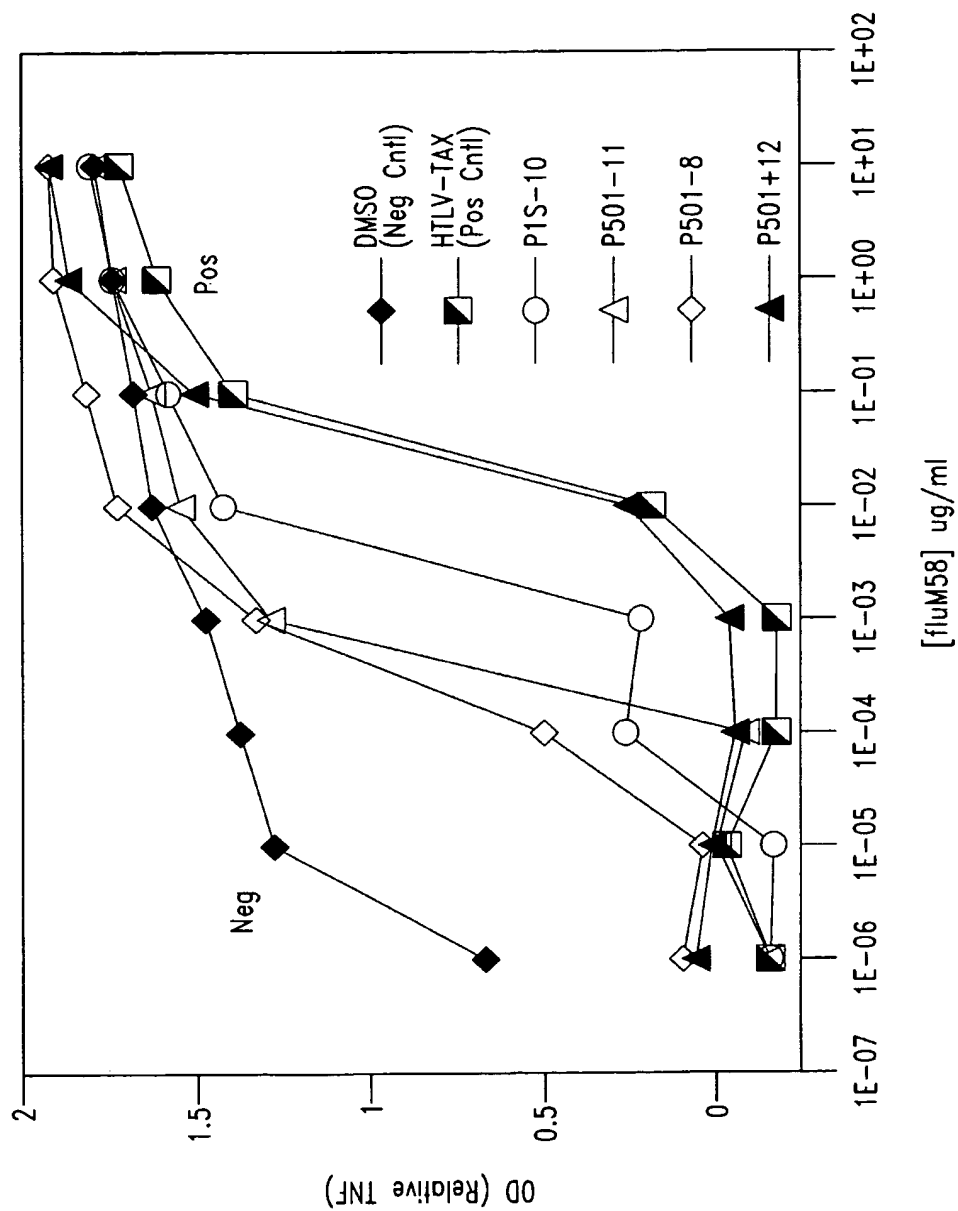
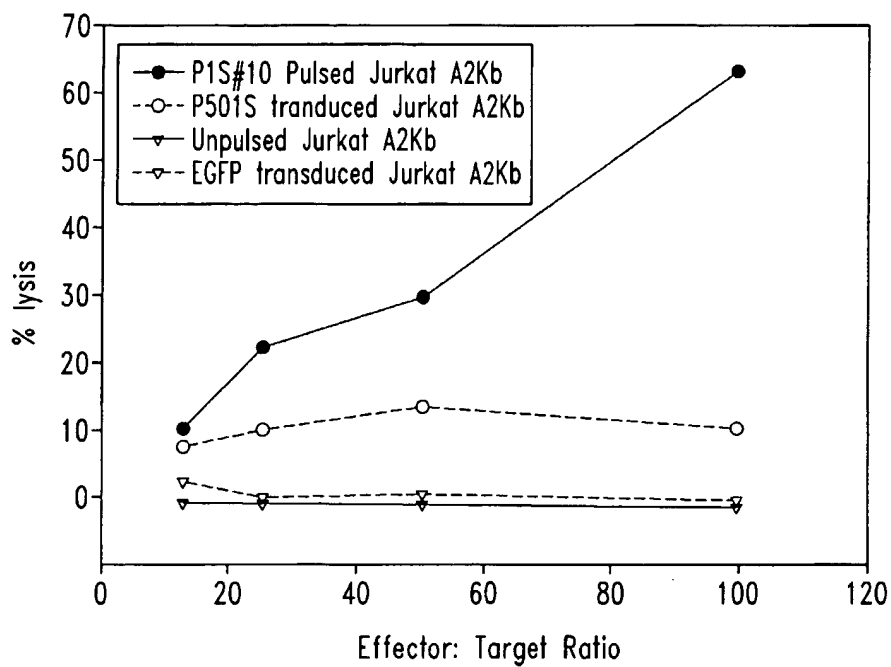
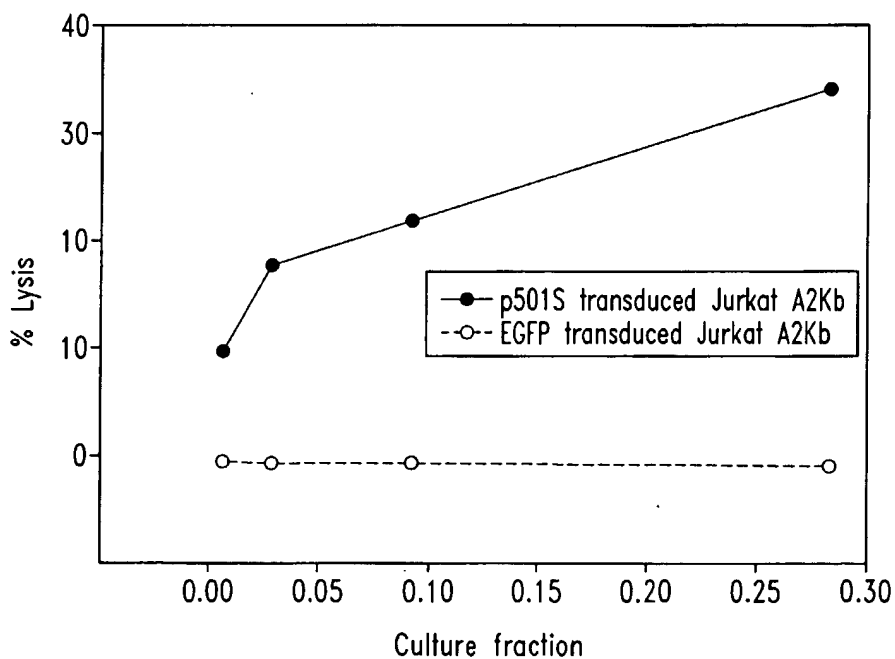
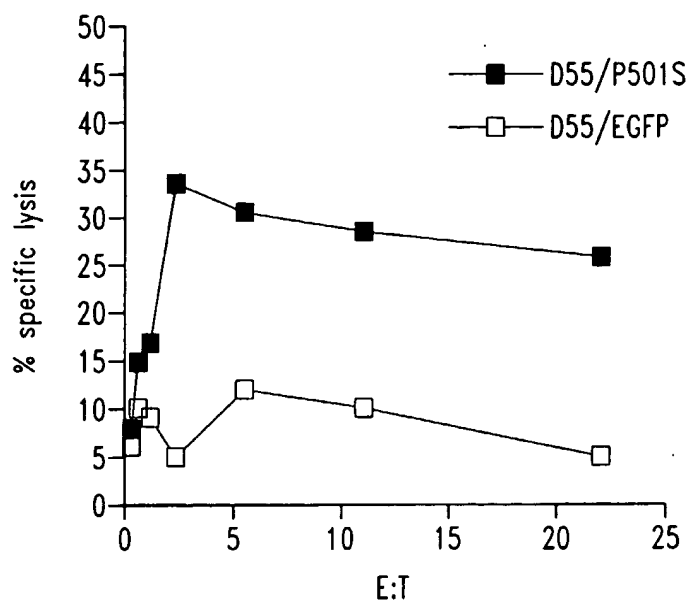
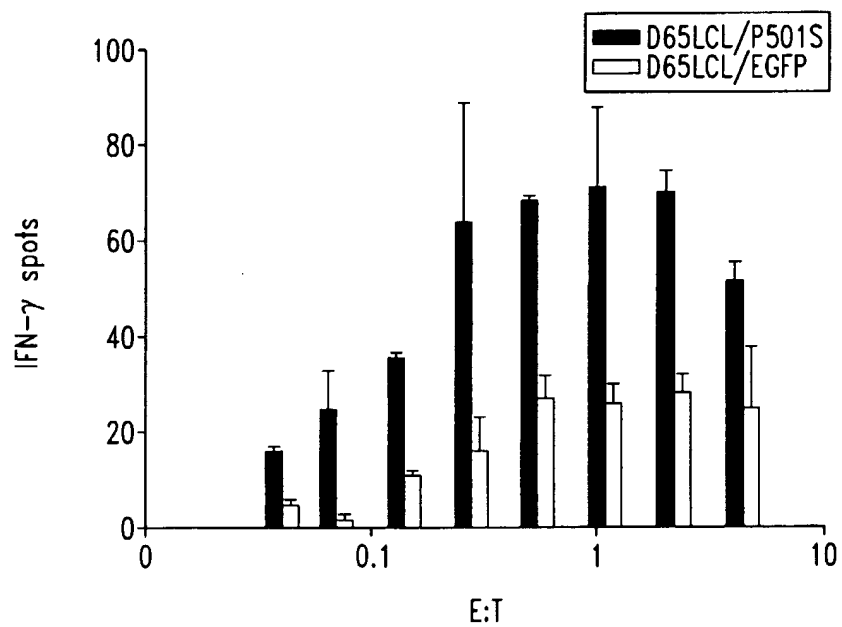
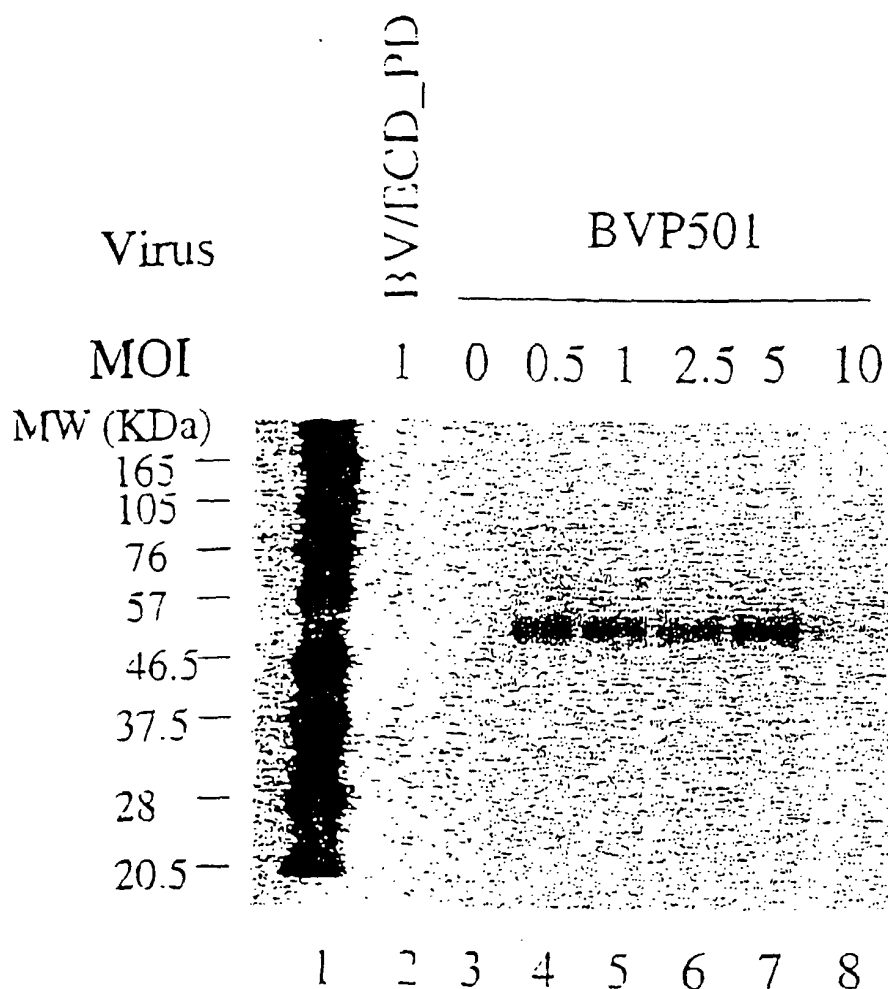


Fig. 3

*Fig. 4**Fig. 5*

*Fig. 6A**Fig. 6B*

Expression of P501S by the Baculovirus Expression System



0.6 million high 5 cells in 6-well plate were infected with an unrelated control virus BV/ECD_PD (lane 2), without virus (lane 3), or with recombinant baculovirus for P501 at different MOIs (lane 4 - 8). Cell lysates were run on SDS-PAGE under the reducing conditions and analyzed by Western blot with a monoclonal antibody against P501S (P501S-10E3-G4D3). Lane 1 is the biotinylated protein molecular weight marker (S.Labs).

Fig. 7

Schematic of P501S with predicted
transmembrane, cytoplasmic, and extracellular regions

MVQRLWVSRLLRHK AQLLLVNLLTFGLEVCLAAGIT **YVPPLLLLEVGVEEKFM**
TMVLGIGPVLGLVCYPLLGSAS
 DHWRGRYGRRRP FIWALSGLILLSFLIPRAGWL AGLLCPDPRPLE LALLILGVGLLDFCGQVCFTPL
 EALLSDLFRDPDHCRQ AYSVYAFMISLGGCLGYLLPAI **DWDT**SALAPYLGTQEE
CLFGLLTILFLTCVAATLLV AEEAALGPTEPAEGLSAPSLSPHCCPCRARLAFRNLGALLPRL
 HQLCCRMPTLRR LFVAELCSWMALMTFTLFYTDF VGEGLYQGVPRAE**PGTEARRHYDEGVR**
MGSLGLFLQCAISLVFSLVM DRLVQRFGTRAVYLAS VAAFPVAAGATCLSHSVAVVTA **SAA**
LTGFTFSALQILPYTLASLY *HREKQVFLPKYRGDTGGASSED*SLMTSFLPGPKPGAPFPNGHVGAGGSGL
*LPPPPALCGASACDVS*VRVVVGEPTEARVVPGRG ICLDLAILDSAFLLSQVAPSLF **MGSIVQLSQS**
VTAYMVSAAGLGLVAIYFAT *QVVF***DKSDLAKYSA**

Underlined sequence: Predicted transmembrane domain; **Bold sequence**:
 Predicted extracellular domain; *Italic sequence*: Predicted intracellular
 domain. Sequence in bold/underlined: used generate polyclonal rabbit
 serum

Localization of domains predicted using HMMTOP (G.E. Tusnady and I. Simon
 (1998) Principles Governing Amino Acid Composition of Integral Membrane
 Proteins; Applications to topology Prediction. J. Mol Biol. 283, 489-506.

Fig. 9

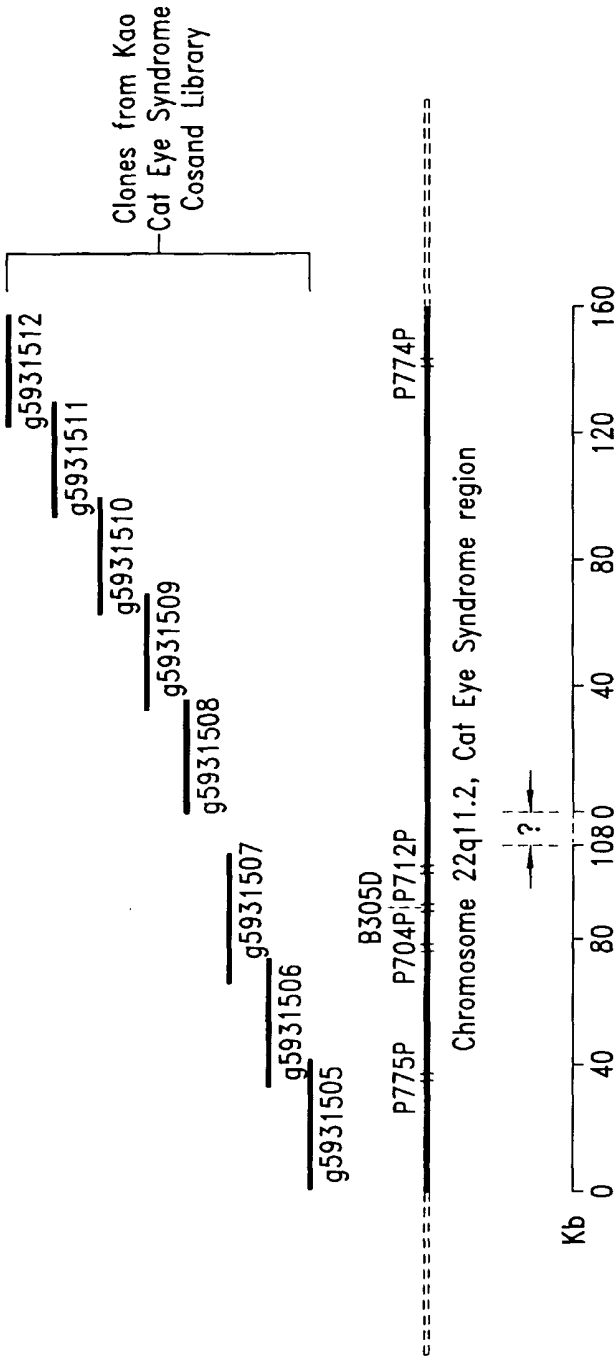


Fig. 10

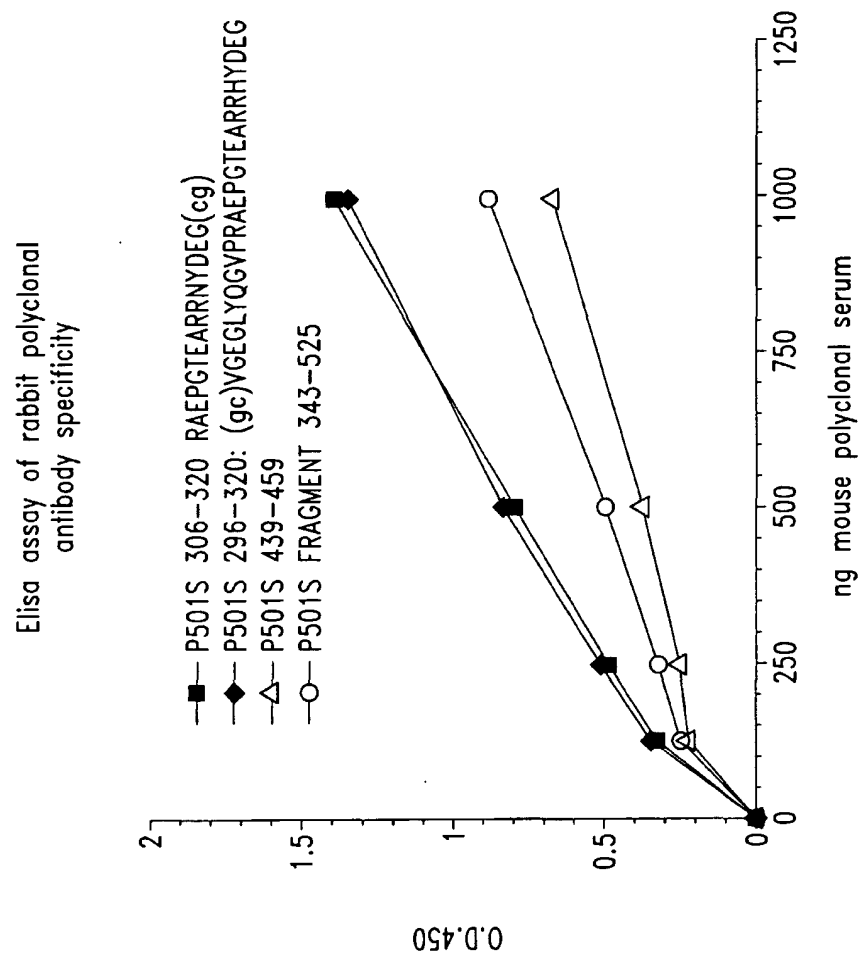


Fig. 11

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 Xu, Jiangchun
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 Harlocker, Susan Louise
 Jiang Yuqui
 Reed, Steven G.
 Kalos, Michael
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<120> COMPOSITIONS AND METHODS FOR THE THERAPY AND
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tctttgangt	gagcccatg	tccatctggg	ccactgtcng	gaccaccttt	ngggagtgtt	480
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caagnccctgn	atccactnnt	nctanaaccg	gcncncnccg	cngtggaaacc	cnccttntgt	600
tccttttct	tnagggttaa	tnnccgcttg	gccttnccan	ngtccnccnc	nttttccnnt	660

```

gttnaaattg ttangenccc nccnntcccn cnnnnnnan cccgaccenn annttnnann 720
ncctgggggt nccnnngat tgaccenncc nccctntant tgcnttnggg nncnntgccc 780
ctttccctct nggganncg 799

```

```

<210> 9
<211> 801
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (801)
<223> n = A,T,C or G

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<400> 9
acgccttgat cctcccaggc tgggactggg tctgggagga gccgggcatg ctgtgggttg 60
taangatgac actcccaaag gtggtcctga cagtggccca gatggacatg gggctcacct 120
caaggacaag gccaccagg gtggggggccg aagccacat gatccttact ctatgagcaa 180
aatccctgt gggggttct ccttgaagtc cgccancagg gctcagtctt tggaccang 240
caggtcatgg ggttgtngnc caactggggg ccncaacgca aaanggcna gggcctcngn 300
caccatccc angacgcggc tacactnctg gacctccnc tccaccactt tcatgcgctg 360
ttentacccg cgnatntgtc ccantgttt cngtgcenac tccantctt nggacgtgcg 420
ctacatacgc cggantcnc nctcccgtt tgctccctatc cagtnccan caacaaattt 480
cncntantg caccnatcc cacttttnc agntttcnc nncngcttc cttntaaaag 540
ggttganccc cggaaaatnc cccaaagggt gggggccngg tacccaactn cccctnata 600
gctgaantcc ccataccnn gntcnatgg ancentcnt tttaannacn ttctnaactt 660
gggaanance ctcgncntn ccccnttaa tccnccctg cnangnnent ccccnntcc 720
nccnnntng gcntntnann cnaaaaaggc cennnancaa tctcctnnn cctcantteg 780
ccanccctcg aaatcgccn c 801

```

```

<210> 10
<211> 789
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (789)
<223> n = A,T,C or G

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```

<400> 10
cagtctatnt ggccagtgtg gcagctttcc ctgtggctgc cgggtgccaca tgectgtccc 60
acagtgtggc cgtggtgaca gcttcagccg ccctcacccg gttcaccttc tcagccctgc 120
agatcctgcc ctacacactg gcctccctct accaccggga gaagcagggt ttcttgccca 180
aataccgagg ggacactgga ggtgctagca gtgaggacag cctgatgacc agcttcctgc 240
cagggcctaa gcctggagct ccctcccta atggacacgt ggggtgctgga ggcagtggcc 300
tgctcccacc tccaccgcg ctctgcgggg cctctgcctg tgatgtctcc gtacgtgtgg 360
tgggtgggtga gccaccgan gccagggtgg ttccggggccg gggcatctgc ctggacctcg 420
ccatcctgga tagtgcttcc tgctgtccca ngtggcccca tccctgttta tgggtcccat 480
tgctcagctc agccagtctg tcaactgcta tatggtgtct gccgcaggcc tgggtctggg 540
cccatttact ttgctacaca ggtantattt gacaagaacg anttggccaa atactcagcg 600
ttaaaaaatt ccagcaacat tgggggtgga aggcctgcct cactgggtcc aactccccgc 660
tctgtttaac ccatggggc tgccggcttg gccgccaatt tctgttgctg ccaaantnat 720
gtggctctct gctgccacct gttgctggct gaagtgcnta cngcncanct nggggggtng 780
gnggttccc 789

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<210> 11
<211> 772

```

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(772)

<223> n = A,T,C or G

<400> 11

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ccccaccctac ccaaataatta gacaccaaca cagaaaagct agcaatggat tcccttctac      60
tttggttaaat aaataagtta aatattttaa tgctgtgtgc tctgtgatgg caacagaagg      120
accaacaggc cacatcctga taaaaggtaa gaggggggtg gatcagcaaa aagacagtgc      180
tgtgggctga ggggacctgg ttcttgtgtg ttgccccca ggactcttcc cctacaaata      240
actttcatat gttcaaatcc catggaggag tgtttcatcc tagaaactcc catgcaagag      300
ctacattaaa cgaagctgca ggttaagggg cttanagatg ggaaaccagg tgactgagtt      360
tattcagctc ccaaaaaccc ttctctaggt gtgtctcaac taggaggcta gctgttaacc      420
ctgagcctgg gtaatccacc tgcagagtc cgcattcca gtgcatggaa cccttctggc      480
ctccctgtat aagtccagac tgaaccccc ttggaaggnc tccagtcagg cagccctana      540
aactggggaa aaaaagaaa gacgccccan cccccagctg tgcantactg cacctcaaca      600
gcacagggtg gcagcaaaaa aaccacttta ctttggcaca aacaaaaact ngggggggca      660
accccggcac ccnangggg gttaacagga ancngggnaa cntggaaccc aattnaggca      720
ggccnccac ccnaatntt gctgggaaat ttttcctccc ctaaattntt tc      772

```

<210> 12

<211> 751

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(751)

<223> n = A,T,C or G

<400> 12

```

gccccaatc cagctgccac accacccacg gtgactgcat tagttcggat gtcatacaaa      60
agctgattga agcaaccctc tacttttttg tcgtgagcct tttgcttggg gcaggtttca      120
ttggctgtgt tggtagcgtt gtcatgtcaa cagaatgggg gaaaggcact gttctctttg      180
aagtanggtg agtcctcaaa atccgtatag ttggtgaagc cacagcactt gagcccttcc      240
atggtgggtg tccacacttg agtgaagtc tccctgggaac cataatcttt cttgatggca      300
ggcactacca gcaacgtcag ggaagtgtc agccattgtg gtgtacacca aggcgaccac      360
agcagctgcn acctcagcaa tgaagatgan gaggangatg aagaagaacg tcncgagggc      420
acacttgctc tcagtcttan caccatanca gcccntgaaa accaananca aagaccacna      480
cnccggctgc gatgaagaaa tnaccccneg ttgacaaact tgcatggcac tggganccac      540
agtggccnna aaaatcttca aaaaggatgc cccatcnatt gaccccccaa atgcccactg      600
ccaacagggg ctgccccacn cncnnaacga tganccnatt gnacaagatc tnentggctc      660
tnatnaacnt gaaccctgcn tngtggctcc tggtcaggnc cnnggcctga cttctnaann      720
aangaactcn gaagncceca cngganannc g      751

```

<210> 13

<211> 729

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(729)

<223> n = A,T,C or G

<400> 13

gagccaggcg	tccctctgcc	tgcccactca	gtggcaacac	ccgggagctg	ttttgtcctt	60
tgtggancct	cagcagtncc	ctctttcaga	actcantgcc	aaganccctg	aacaggagcc	120
accatgcagt	gcttcagctt	cattaagacc	atgatgatcc	tcttcaattt	gtcatctttt	180
ctgtgtggtg	cagccctggt	ggcagtgggc	atctgggtgt	caatcgatgg	ggcatccttt	240
ctgaagatct	tggggccact	gtcgtccagt	gccatgcagt	ttgtcaacgt	gggctacttc	300
ctcatcgagc	ccggcggtgt	ggtcttagct	ctaggtttcc	tgggctgcta	tgggtgctaag	360
actgagagca	agtgtgccct	cgtgacgttc	ttcttcatcc	tcctcctcat	cttcattgct	420
gagggtgcaa	tgctgtggtc	gccttgggtg	acaccacaat	ggctgagcac	ttcctgacgt	480
tgctggtaat	gcctgccatc	anaaaaagat	tatgggttcc	cagggaanact	tcactcaagt	540
gttggaacac	caccatgaaa	gggctcaagt	gctgtggctt	cnnccaacta	tacggatttt	600
gaagantcac	ctacttcaaa	gaaaanagtg	cctttccccc	atttctgttg	caatgacaa	660
acgtcccaaa	cacagccaat	tgaaaacctg	cacccaaccc	aaanggggtc	ccaaccanaa	720
attnaagg						729

<210> 14

<211> 816

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (816)

<223> n = A,T,C or G

<400> 14

tgctcttctt	caaagttggt	cttgttgcca	taacaaccac	cataggtaaa	gcggggcgag	60
tggtcgctga	aggggttgta	gtaccagcgc	gggatgctct	ccttgcagag	tcctgtgtct	120
ggcaggtcca	cgcagtggcc	tttgtcactg	gggaaatgga	tgcgctggag	ctcgtcaaag	180
ccactcgtgt	atttttcaca	ggcagcctcg	tcgcagcgtg	cggggcagtt	gggggtgtct	240
tcacactcca	ggaactgtc	natgcagcag	ccattgctgc	agcggaaactg	ggtgggctga	300
cangtgccag	agcacactgg	atggcgccct	tccatgnnan	gggccctgng	ggaaagtccc	360
tganccecan	anctgcctct	caaangcccc	accttgcaac	ccccgacagg	ctagaatgga	420
atcttcttcc	cgaaggttag	ttnttcttgt	tgcccaance	anccccntaa	acaaactctt	480
gcanatctgc	tccgnggggg	tentantacc	anegtgggaa	aagaacccca	ggcngcgaac	540
caancttggt	tggatncgaa	gnataatct	ncnttctg	ttggtggaca	gcaccantna	600
ctgtnnanct	ttagnccntg	gtcctcntgg	gttgnncttg	aacctaatcn	ccnntcaact	660
gggacaaggt	aantngccnt	cctttnaatt	cccnanctn	ccccctggtt	tgggggtttt	720
cncnctccta	ccccagaaan	ncctgtgttc	cccccaacta	ggggccnaaa	ccnnttnttc	780
cacaaccctn	ccccaccac	gggttcngnt	ggttng			816

<210> 15

<211> 783

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (783)

<223> n = A,T,C or G

<400> 15

ccaaggcctg	ggcaggcata	nacttgaagg	tacaacccca	ggaacccctg	gtgctgaagg	60
atgtggaaaa	cacagattgg	cgctactg	ggggtgacac	ggatgtcagg	gtagagagga	120
aagacccaaa	ccaggtggaa	ctgtggggac	tcaaggaang	cacctacctg	ttccagctga	180
cagtgactag	ctcagaccac	ccagaggaca	cggccaacgt	cacagtcact	gtgctgtcca	240
ccaagcagac	agaagactac	tgctcgcac	ccaacaangt	gggtcgctgc	cggggctctt	300
tcccacgctg	gtactatgac	cccacggagc	agatctgcaa	gagtttcgtt	tatggaggct	360

gcttgggcaa	caagaacaac	taccttcggg	aagaagagt	cattctance	tgtcnggggtg	420
tgcaagggtg	gcctttgana	ngcanctctg	gggctcangc	gactttcccc	cagggcccct	480
ccatggaaag	gcgccatcca	ntgttctctg	gcacctgtca	gcccacccag	ttccgctgca	540
ncaatggctg	ctgcactcnac	antttcctng	aattgtgaca	acacccccca	ntgcccccaa	600
ccctcccaac	aaagcttccc	tgtnnaaaaa	tacnccantt	ggcttttnac	aaacncccg	660
cnctcctntt	ttcccnntn	aacaaagggc	nctngcnttt	gaactgccc	aaccnnggaa	720
tcnccnngg	aaaaantncc	ccccctggtt	cctnnaance	cctccnnaa	anctncccc	780
ccc						783

<210> 16
 <211> 801
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (801)
 <223> n = A,T,C or G

<400> 16						
gccccaatc	cagctgccac	accacccacg	gtgactgcat	tagttcggat	gtcatacaaa	60
agctgattga	agcaaccctc	tacttttttg	tcgtgagcct	tttgcttggt	gcaggtttca	120
ttggtgtgt	tggtgacgtt	gtcattgcaa	cagaatggg	gaaaggcact	gttctctttg	180
aagtaggggtg	agtcctcaaa	atccgtatag	ttggtgaagc	cacagcactt	gagccctttc	240
atggtgggtg	tccacacttg	agtgaagtct	tcctgggaac	cataatcttt	cttgatggca	300
ggcactacca	gcaacgtcag	gaagtgtc	gccattgtgg	tgtacaccaa	ggcgaccaca	360
gcagctgcaa	cctcagcaat	gaagatgagg	aggaggatga	agaagaacgt	cncgagggca	420
cacttgctct	ccgtcttagc	accatagcag	cccangaaac	caagagcaaa	gaccacaacg	480
ccngetgcga	atgaaagaaa	ntaccacagt	tgacaaactg	catggccact	ggacgacagt	540
tgccccgaan	atcttcagaa	aagggatgcc	ccatcgattg	aacacccana	tgcccactgc	600
cnacagggct	gcncncn	gaaagaatga	gccattgaag	aaggatcntc	ntggtcttaa	660
tgaactgaaa	ccntgcatgg	tgccccctgt	tcagggtctt	tggcagtga	ttctganaaa	720
aaggaacngc	ntnagcccc	ccaaangana	aaacaccccc	gggtgttgcc	ctgaattggc	780
ggccaaggan	ccctgccccn	g				801

<210> 17
 <211> 740
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (740)
 <223> n = A,T,C or G

<400> 17						
gtgagagcca	ggcgtccctc	tgctgcccc	ctcagtggca	acacccggga	gctgttttgt	60
cctttgtgga	gcctcagcag	ttccctcttt	cagaactcac	tgccaagagc	cctgaacagg	120
agccaccatg	cagtgttca	gcttcattaa	gaccatgatg	atcctcttca	atttgctcat	180
ctttctgtgt	ggtgcagccc	tggtggcagt	gggcatctgg	gtgtcaatcg	atggggcatc	240
ctttctgaag	atcttcgggc	cactgtcgtc	cagtgccatg	cagtttgtca	acgtgggcta	300
cttctcatc	gcagccggcg	ttgtggtctt	tgctcttggt	ttcctgggct	gctatggtgc	360
taagacggag	agcaagtgtg	ccctcgtgac	gttcttcttc	atcctcctcc	tcattctcat	420
tgctgaagtt	gcagctgctg	tggtcgctt	gggtgtacac	acaatggctg	aaccattcct	480
gacgttgctg	gtantgcctg	ccatcaanaa	agattatggg	ttcccaggaa	aaattcactc	540
aantntggaa	caccnccatg	aaaagggtc	caatttctgn	tggttcccc	aactataccg	600
gaattttgaa	agantcnccc	tacttccaaa	aaaaaanant	tgcttttnc	ccnttctgt	660
tgcaatgaaa	acntcccaan	acngccaatn	aaaacctgcc	cnnncaaaaa	ggntcncaaa	720

caaaaaaant nnaagggttn

740

<210> 18
 <211> 802
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)... (802)
 <223> n = A,T,C or G

<400> 18
 ccgctggttg cgctggtcca gngnagccac gaagcacgtc agcatacaca gcctcaatca 60
 caaggtcttc cagctgccgc acattacgca gggcaagagc ctccagcaac actgcatatg 120
 ggatacactt tacttttagca gccagggtga caactgagag gtgtcgaagc ttattcttct 180
 gagcctctgt tagtggagga agattccggg cttcagctaa gtagtcagcg tatgtcccat 240
 aagcaaacac tgtgagcagc cggaaggtag aggcaaagtc actctcagcc agctctctaa 300
 cattgggcat gtccagcagt tctccaaaca cgtagacacc agnggcctcc agcacctgat 360
 ggatgagtgt ggccagcgct gcccccttgg ccgacttggc taggagcaga aattgtcctc 420
 ggttctgccc tgtcaccttc acttccgcac tcatcactgc actgagtgtg ggggacttgg 480
 gctcaggatg tccagagacg tggttccgcc ccctcnctta atgacaccgn ccanncaacc 540
 gtcggctccc gccgantgng ttcgtcgtnc ctgggtcagg gtctgtctggc cncacttgc 600
 aancttcgtc nggcccatgg aattcacnc accggaactn gtangatcca ctnttctat 660
 aaccgngcgc caccgcnntt ggaactccac tctnttnc tttacttgag ggtaaggtc 720
 acccttnncg ttaccttggc ccaaaccntn ccntgtgtcg anatngtnaa tcnggncna 780
 tnccancnc atangaagcc ng 802

<210> 19
 <211> 731
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)... (731)
 <223> n = A,T,C or G

<400> 19
 cnaagcttcc aggtnacggg ccgnaance tgaccnagg tancanaang cagnncgcgg 60
 gagcccaccg tcacnggng gngtctttat nggagggggc ggagccacat cncctggacnt 120
 cntgacccca actcccncc nncantgca gtgatgagtg cagaactgaa ggtnacgtgg 180
 caggaaccaa gancaaannc tgetcnntc caagtcggcn nagggggcgg ggctggccac 240
 gcncatccnt cnagtgtcgn aaagcccn cctgtctact tgtttgaga acngcnnga 300
 catgcccagn gttanataac ngcngagag tnantttgc tctccctcc ggctgcgan 360
 cgngtntgct tagnggacat aacctgacta cttaactgaa ccnngaate tncnccct 420
 cactaagct cagaacaaaa aacttcgaca ccactcantt gtcacctgnc tgctcaagta 480
 aagtgtaccc catncccaat gtntgctnga ngetctgnc tgcnttangt tcggtcctgg 540
 gaagacctat caattnaagc tatgtttctg actgcctctt gctccctgna acaancc 600
 cnnnntcca agggggggnc ggcccccaat ccccccaacc ntnaattnan ttancccn 660
 ccccnnggcc cggcctttta cnancntenn nnaengggna aaaccnnngc ttncccaac 720
 nnaatecncc t 731

<210> 20
 <211> 754
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(754)
 <223> n = A,T,C or G

<400> 20
 . tttttttttt tttttttttt taaaaacccc ctccattnaa tgnaaacttc cgaaattgtc 60
 caaccccctc ntccaaatnn ccttttcggt gnggggggttc caaacccaan ttannttttg 120
 annttaaaatt aaatnttntt tggnggnnna anccnaatgt nangaaagtt naaccanta 180
 tnancttnaa tncctggaaa ccngtngntt ccaaaaatnt ttaaccctta antccctccg 240
 aaatngtttna nggaaaaccc aantttctnt aaggttggtt gaaggntnaa tnaaaanccc 300
 nnccaattgt ttttngccac gctgaatta attggnnttc gntgttttcc nttaaaanaa 360
 ggnnancccc gggtantnaa tccccccnnc cccaattata ccganttttt ttngaattgg 420
 gancccnccg gaattaacgg ggnnnntccc tnttgggggg cnggnncccc ccccntcggg 480
 ggttngggnc aggnncnaat tgtttaaggg tccgaaaaat ccctccnaga aaaaaanctc 540
 ccaggntgag nntnggggtt ncccccccc canggccctt ctognanagt tggggtttgg 600
 ggggcctggg attttntttt cctntttnc tcccccccc ccnggganag aggttngngt 660
 tttgntcncn ggcncncn aaganctttn ccganttnan ttaaatccnt gcctnggcga 720
 agtccnttgn agggntaaan ggccccctnn cggg 754

<210> 21
 <211> 755
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(755)
 <223> n = A,T,C or G

<400> 21
 atcancat gaccccaac nngggaccnc tcancggnc nnnnacnc cggccnatca 60
 nngtnagnnc actncnnttn natcacnccc cncnactac gccncnanc cnacgcnc 120
 nncanctncc actganngcg cgangtngan ngagaaanct nataccanag ncaccanacn 180
 ccagctgtcc nanaangcct nnnatacngg nnnatccaat ntgnancctc cnaagtattn 240
 nncnncanct gattttccctn anccgattac cctncccc tanccctcc ccccaacna 300
 cgaaggcncct ggncncaagg nngcgncc cgcgtagntc ccnncnaagt cncncncc 360
 aactcancn nattaacgc ttentgagta tcaactcccg aatctcacc tactcaactc 420
 aaaaanactn gatacaaat aatncaagc tgnattatnac actntgactg ggtctctatt 480
 ttagnggtcc ntnaanctc ctaatacttc cagtctncc tcnccaattt ccnaanggct 540
 ctttcngaca gcatnttttg gttcccnntt ggggtcttan ngaattgcc ttctnngaac 600
 gggtcctct tttccttcgg ttanctggg tcnncggc cagttattat ttccntttt 660
 aaattcctnc cttttanttt tggctttna aaccccggc cttgaaaacg gcccctggg 720
 aaaagggtgt tttganaaaa tttttgtttt gttcc 755

<210> 22
 <211> 849
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(849)
 <223> n = A,T,C or G

<400> 22
 tttttttttt tttttangtg tngtcgtgca ggtagaggt tactacaant gtgaanacgt 60
 acgctnggan taangcgacc cgantttctag gannccct aaaaatcanac tgtgaagatn 120

```

atcctgnna  cggaanggtc  accggnngat  nntgctaggg  tgneenctcc  kannncttn  180
cataactcng  nggccctgcc  caccaccttc  ggcggeccng  ngnccgggcc  cgggtcattn  240
gnnttaaccn  cactnngcna  neggtttccn  nccccnncng  acccnggcga  tccggggtnc  300
tetgtcttcc  cctgnagncn  anaaantggg  ccncggncce  ctttaccct  nnacaagcca  360
cngccntcta  nccncngccc  cccctccant  nngggggact  gecnanngct  ccgttntng  420
nnaccccnnn  gggtncctcg  gttgtcgant  cnaccgnang  ccanggattc  cnaaggaagg  480
tgcgttnttg  gcccctaccc  ttegtncggy  nncaccttc  ccgacnanga  nccgtcccg  540
cnncnngnng  cctcncctcg  caacacccgc  nctctcngt  nccggnnccc  cccacccgc  600
nccctcncnc  ngncgnancn  ctcncncnc  gtctcannca  ccaccccgcc  ccgccaggcc  660
ntcanccacn  ggnngacnng  nagnccntc  gcncgcgcn  gcgncnccct  cgcncngaa  720
ctnctcngg  ccantnncgc  tcaanccna  cnaaacgcc  ctgcgcggcc  cgnagcgnc  780
nccctcncga  gtctcccg  cttccnacc  angnttccn  cgaggacacn  nnaccccgcc  840
nncangcgg

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<210> 23
<211> 872
<212> DNA
<213> Homo sapien

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<220>
<221> misc_feature
<222> (1)...(872)
<223> n = A,T,C or G

```

```

<400> 23
gagcaacta  tacttegtc  gnactcgtc  gcctcgtnc  tcttttctc  cgcaaccatg  60
tgtgacnanc  ccgattngc  ngatatcnan  aagntcganc  agtccaaact  gantaacaca  120
cacacnncn  aganaaatcc  nctgccttc  anagtancn  attgaacnng  agaaccangc  180
nggcgaateg  taatnaggcg  tgcgccgcca  atntgtcncc  gtttatttn  ccagctcnc  240
ctnccnacc  taentcttc  nagctgtcnn  accctngtn  cgnaccccc  naggtcggga  300
tcgggtttnn  nntgaccgng  cnnccccct  cccctccat  nacgancnc  ccgcaccacc  360
nanngcncg  nccccgnc  cttegcnc  ctgtccttn  cccctgtng  ctggcncngn  420
accgcattga  cctcgcenn  ctncnngaaa  ncgnanacgt  ccgggttggn  annancgctg  480
tggnnnngcg  tetgcncgc  gttccttcn  ncnncttcca  ccattctct  taenggtct  540
ccncgcctc  tcnncacnc  cctgggacgc  tntcctntg  ccccttnac  tccccctt  600
cgncgtgnc  cgnccccacc  ntcatttnca  nacgntcttc  acaannncc  ggntnnctc  660
cnancngcn  gtcanccnag  ggaagggng  ggnncnntg  nttagcgtg  ngngangtc  720
cgaanantcc  tcnccntcan  cctaccctc  cggcggnnc  ctngttnc  aacttanca  780
ntctccccg  ngngcncnc  tcagcctcnc  cccccnct  ctctgcantg  tctctgctc  840
tnaccnntac  gantnttcg  cncctctt  cc

```

```

<210> 24
<211> 815
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(815)
<223> n = A,T,C or G

```

```

<400> 24
gcatgcaagc  ttgagtattc  tatagngtca  cctaaatanc  ttggcntaat  catggtcnta  60
nctgncttcc  tgtgtcaaat  gtatacnaa  tanatatgaa  tctnatntga  caaganngt  120
tcntncatta  gtaacaantg  tnntgtccat  cctgtcngan  canattccca  tnnattncgn  180
cgcattcnnc  gencantatn  taatngggaa  ntcnnntnn  ncacnncat  ctatctncc  240
gncctgac  tggagagat  ggatnanttc  tnntntgacc  nacatgttca  tcttgattn  300
aanaccccc  cgcngnccac  cggttngnng  cnagcncntc  ccaagacctc  ctgtggaggt  360

```

aacctgcgtc	aganncatca	aacntgggaa	accgcgnccc	angtnnaagt	ngnnncanan	420
gaccccgccc	aggnttnacc	atcccttcnc	agcgcceccc	ttngtgccct	anagngnagc	480
gtgtccnanc	cnetcaacat	ganacgegcc	agnccanccg	caattnggca	caatgtcgnc	540
gaaccccccta	gggggantna	tncaaanccc	caggattgtc	cncncangaa	atcccncanc	600
cccnccctac	ccnnctttgg	gacngtgacc	aantcccggg	gtncaggtcc	ggcngnctc	660
ccccaccggt	nncentgggg	gggtgaanct	cngnntcanc	cngncgaggn	ntcgnaagga	720
accggncctn	ggncgaanng	ancnntcnga	agngccnctc	cgtataaacc	cccctcncca	780
nccnacngnt	agntcccccc	cngggtncgg	aangg			815

<210> 25
 <211> 775
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (775)
 <223> n = A,T,C or G

<400> 25	
ccgagatgtc	tcgctccgtg
aggetatcca	gcgtactcca
agtcaaattt	cctgaattgc
tactgaagaa	tgganagaga
actgggtctt	ctatctcntg
cctgcccgtg	gaaccatgtg
tgtaagcagn	cnncatggaa
ctgcttgcct	gcnttttaat
tgtaggggtt	acatnantgt
aattgcccgt	cncccngttn
tcttacggaa	gggcctgggc
ccncccncca	cnntcttgng
nccttnncta	anaaaacttn
gccttagctg	tgctcgcgct
tttactcacg	tcattccagca
ggtttccatc	atccgacatt
tggagcattc	agacttgctc
aattcacccc	cactgaaaaa
agcccaagat	agttaagtgg
gccgcatttg	gattggatga
ntatacaccc	taccctttat
catgatcttc	ctttataant
cnnaaccacg	gttggctccc
ggttggggga	accnaaaatt
ggaacccttc	cnattcccct
naaanntttn	acttcccccc
gatcagatgc	tctggcctgg
gagaatggaa	
gaanttgact	
ttcagcaagg	
gatgagtatg	
gatcgagaca	
attccaaatt	
gnccccaatt	
ccnccnttcg	
ccaggtcncc	
tcncttntgc	
tggcctcnna	
ttacc	

<210> 26
 <211> 820
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (820)
 <223> n = A,T,C or G

<400> 26	
anattantac	agtgtaatct
cccanagata	ncttatanca
gaaaagggtg	cggtccccc
ccatcangcc	ttcggtggga
ntgatgacca	tgggcgggag
nctgaggggt	cacactataa
ttcctacctg	acnaccagn
acnnagcact	cacctgcccc
ccctgttgga	attncgggga
gatggaattt	tncccttcgg
tcctctnttt	ntcctgnenc
ganattccac	tnncgcctnc
gggnnccctg	ntcctcctct
gtgtgtanag	ggaacggggc
gaccaagagc	tgctgggcac
ctcccatagc	catcccagag
gaaacaacan	accacagagc
ccctgnaccg	gggtggcana
ccnagatnan	cacctgcttc
gcngcctggg	gacagcncctg
tnccgntccc	tggtcctgnc
nccccctcct	ccanctgtga
tccttcttta	cacgccccct
ccnnnatttc	ccttnattga
naanaacnaaa	nactntctna
accnccnntt	ctttgcctct
gagagcctgc	ggancagcta
aagggaagct	
aggaaaaann	
nntactctnc	
tcggannctn	
cccnggggat	
ccttngatca	

tccaacntc gntggcctn ccccccnntc tcttttcccc

820

<210> 27
 <211> 818
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(818)
 <223> n = A,T,C or G

<400> 27
 tctgggtgat ggctcttcc tctcagga cctctgactg ctctgggcca aagaatctct 60
 tgtttcttct cggagcccca ggcagcgggtg attcagccct gcccaacctg attctgatga 120
 ctgctgatgc tgtgacggac ccaaggggca aatagggtcc cagggtccag ggaggggcgc 180
 ctgctgagca ctccgcccc tcacctgcc cagccctgc catgagctct gggctgggtc 240
 tccgctcca gggttctgct cttccangca ngccancaa tggcgctggg ccacactggc 300
 ttcttctgc cccntccctg gctctgante tctgtcttcc tgtcctgtgc angcnccttg 360
 gatctcagtt tccctcctc anngaactct gtttctgann tcttcantta actntgantt 420
 tatnaccnan tggnetgtnc tgtcnnactt taatgggcn gaccggctaa tccctccctc 480
 netcccttc anttcnnna accngcttnc cntctctcc centancccg ccnggggaanc 540
 ctcccttgc ctnaccangg gccnnnaccg cccntnctn ggggggcnng gtnnctnenc 600
 ctgntnnccc cncctcncnt tncctcgtcc cncnncgc nngcannttc ncngtcccn 660
 tnnctctcn ngntcgnaa ngntcncntn tnnnnngcn ngntnntcn tccctctcnc 720
 cnnntgnang tnnntnnnc ncngnncccc nnnncnnnn nggnntnnn tctnncngc 780
 cccnncccc ngnattaagg cctcncntct cgggcnc 818

<210> 28
 <211> 731
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(731)
 <223> n = A,T,C or G

<400> 28
 aggaaggcg gagggatatt gtangggatt gagggatagg agnataangg gggaggtgtg 60
 tccaacatg anggtgnngt tctcttttga angagggtg ngtttttann ccnggtgggt 120
 gattnaacc cattgtatgg agnnaaagg ttnagggtat ttttcggctc ttatcagtat 180
 ntanattcct gtnaatcgga aaatnatnt tcnncnggaa aatnttgctc ccatccgnaa 240
 attnctccc ggtagtgcatt nttngggggn cngccangtt tcccaggtg ctanaatcgt 300
 actaaagntt naagtgggan tncaaatgaa aacctnnac agagnatccn tacccgactg 360
 tnnnttncct tcgcccctng actctgcnn agcccaatac ccnngngnat gtncnccngn 420
 nnngegnnc tgaaannnc tcgnggctnn gancatcang gggtttcgca tcaaaagcnn 480
 cgtttncat naaggcactt tngcctcat caaccnctng ccctcnncca tttngccgtc 540
 nggttncct acgctnntng cncctnnntn ganattttnc ccgctnggg naancctct 600
 gnaatggga gggnetntc ttttnaccnn gnggtntact aatcnnctnc acgctnctt 660
 tctnaccce ccccttttt caatcccanc ggcaaatggg gtctcccnn cgangggggg 720
 nnnccannc c 731

<210> 29
 <211> 822
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(822)
 <223> n = A,T,C or G

<400> 29
 actagtccag tgtgggtggaa ttccattgtg ttgggggncnc ttctatgant antnttagat 60
 cgctcanacc tcacancctc ccnacnange ctataangaa nannaataga nctgtncnnt 120
 atntntacnc tcatanncct cnnnacccac tccctcttaa cccntactgt gcctatngcn 180
 tnnctantct ntgccgcctn cnanccaccn gtggggccnac cncnngnatt ctcnatctcc 240
 tenccatntn gcctananta ngtnccatcc ctatacctac nccaatgcta nnnctaancn 300
 tccatnantt annntaacta ccaactgaent ngacttttenc atnanctcct aatttgaatc 360
 tactctgact cccacngcct annnattagc anentcccc nacnatntct caaccaaadc 420
 ntcaacaacc tatctanctg ttcnccaacc nttncctccg atccccnnac aacccccctc 480
 ccaaataccc nccacctgac ncctaaccen caccatcccg gcaagccnan ggnccatttan 540
 ccactgggaat cacnatngga naaaaaaac ccnaactctc tancncnnat ctccctaana 600
 aatnctcctn naatttactn ncantnccat caanccacn tgaaacnnaa cccctgtttt 660
 tanatccctt ctttcgaaaa ccnacccttt annncccaac ctttngggcc cccccnctnc 720
 ccnaatgaag gncncccaat cnangaaacg nccntgaaaa ancnaaggcna anannntccg 780
 canatcctat cccttanttn ggggncctt nccnngggcc cc 822

<210> 30
 <211> 787
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(787)
 <223> n = A,T,C or G

<400> 30
 cggccgcctg ctctggcaca tgccctcctga atggcatcaa aagtgatgga ctgcccattg 60
 ctagagaaga ctttctctcc tactgtcatt atggagccct gcagactgag ggctcccctt 120
 gtctgcagga tttgatgtct gaagtcgtgg agtgtggctt ggagctcctc atctacatna 180
 gctggaagcc ctggagggcc tctctcgcca gccctcccct tctctccacg ctctccangg 240
 acaccagggg ctccaggcag cccattatc ccagnangac atgggtgtttc tccacgcgga 300
 cccatggggc ctgnaaggcc agggctcctt ttgacaccat ctctcccgtc ctgctggca 360
 ggccgtggga tccactantt ctanaacggn cgcacccnng gtgggagctc cagcttttgt 420
 tccnttaat gaaggttaat tgcncgcttg gcgtaatcat nggtcanaac tntttcctgt 480
 gtgaaattgt ttntccccct ncnattccnc ncnacatacn aaccgcggaan cataaagtgt 540
 taaagcctgg gggtngcctn nngaataaac tnaactcaat taattgcgtt ggctcatggc 600
 ccgctttccn ttcnggaaaa ctgtcntccc ctgcnttntt gaatcgcca cccccnggg 660
 aaaagcggtt tgcnttttng ggggntcctt ccnetcccc cctcnctaan cctnccgct 720
 cggtcgttnc nggtngcggg gaangggnat nnnctcccnc naagggggng agnnngntat 780
 ccccaaa 787

<210> 31
 <211> 799
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(799)
 <223> n = A,T,C or G

<400> 31

```

tttttttttt tttttttggc gatgctactg ttttaattgca ggaggtgggg gtgtgtgtac      60
catgtaccag ggctattaga agcaagaagg aaggagggag ggcagagcgc cctgctgagc      120
aacaaaggac tctgcagcc ttctctgtct gtctcttggc gcaggcacat ggggaggcct      180
cccgagggt gggggccacc agtccagggg tgggagcact acanggggtg ggagtgggtg      240
gtggctggtn cnaatggcct gncacanatc cctacgattc ttgacacctg gatttcacca      300
ggggaccttc tgttctccca nggnaacttc nttnnatctn aaagaacaca actgtttctt      360
cngcanttct ggctgttcat ggaaagcaca ggtgtccnat ttnggctggg acttgggtaca      420
tatggttccg gcccacctct cccntcnaaa aagtaattca ccccccccn cctctnttg      480
cctgggccct taantaccca caccggaact canttantta ttcattctng gntgggcttg      540
ntnatcnccn cctgaangcg ccaagttgaa aggccacgcc gtncccnctc cccatagnan      600
nttttnnctn canctaagc cccccnggc aacnatccaa tcccccccn tgggggcccc      660
agcccgaggc ccccgntctg gggnnccngn cncgnantcc ccaggntctc ccantcngnc      720
ccnnngcncc cccgcacgca gaacanaagg ntngagcnc cgcannnnnn nggtnnncac      780
ctcgccccc ccnncgngg

```

```

<210> 32
<211> 789
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (789)
<223> n = A,T,C or G

```

```

<400> 32
tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt      60
ttttnccnag ggcaggttta ttgacaacct cncgggacac aancaggctg gggacaggac      120
ggcaacaggc tccggcgcg gcgcgcgcg cctacacctg ggtaccaaat ntgcagcctc      180
cgctcccgct tgatnttct ctgcagctgc aggatgcctt aaaacagggc ctcggcctn      240
ggtgggcacc ctgggatttn aatttccacg ggcacaatgc ggtcgcancc cctcaccacc      300
nattaggaat agtggnttta ccnccnccg ttggcncact cccnttgaa accacttntc      360
gcggctccgg catctggtct taaaccttgc aaacnctggg gccctctttt tggttantnt      420
nccngccaca atcatnactc agactggcnc gggctggccc caaaaaancc ccccaaaacc      480
ggncatgtc ttnccggggt tgctgcnatn tncatcacct cccgggcnc nccaggncaac      540
ccaaaagtgc ttgnggccn caaaaaanct cgggggggnc ccagtttcaa caaagtcac      600
ccccttgccc cccaaatcct cccccgntt nctgggtttg ggaaccacg cctctnnctt      660
tggnnggcaa gntggntccc ccttcgggcc cccggtgggc ccnctctaa ngaaaaacnc      720
ntcctnnnca ccatccccc nngnnacgnc tancaangna tccctttttt tanaaacggg      780
ccccccncc

```

```

<210> 33
<211> 793
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (793)
<223> n = A,T,C or G

```

```

<400> 33
gacagaacat gttggatggt ggagcacctt tctatacgac ttacaggaca gcagatgggg      60
aattcatggc tgttggagca atanaacccc agttctacga gctgctgac aaaggacttg      120
gactaaagtc tgatgaactt cccaatcaga tgagcatgga tgattggcca gaaatgaana      180
agaagtttgc agatgtatth gcaaagaaga cgaaggcaga gtggtgtcaa atctttgacg      240
gcacagatgc ctgtgtgact cgggttctga cttttgagga ggttgttcat catgatcaca      300
acaangaacg gggctcgtht atcaccantg aggagcagga cgtgagcccc cgccctgcac      360

```


ctctgctgtt	aaacacccca	gccatccctt	ctttcaaaag	ggatccacta	cttctagagc	420
ggnccgccacc	gcggtggagc	tccagctttt	gttcccttta	gtgaggggta	attgcgcgct	480
tggcgtaatc	atgggtcatan	ctgtttcctg	tgtgaaattg	ttatccgctc	acaattccac	540
acaacatacg	anccggaagc	atnaaatttt	aaagcctggn	ggtngcctaa	tgantgaact	600
nactcacatt	aattggcttt	gcgctcactg	cccgttttcc	agtcgggaaa	acctgtcctt	660
gccagctgcc	nttaatgaat	cnngccaccc	cccggggaaa	aggcngtttg	cttnttgggg	720
cgcncttccc	gctttctcgc	ttcctgaant	ccttcccccc	ggtctttcgg	cttgccggcna	780
acggtatcna	cct					793

<210> 34

<211> 756

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(756)

<223> n = A,T,C or G

<400> 34

gccgcgaccg	gcatgtacga	gcaactcaag	ggcgagtggg	accgtaaaag	ccccaatctt	60
ancaagtgcg	gggaanagct	gggtcgactc	aagctagtcc	ttctggagct	caacttcttg	120
ccaaccacag	ggaccaagct	gaccaaacag	cagctaattc	tggcccgtag	catactggag	180
atcgggggccc	aatggagcat	cctacgcaan	gacatcccct	ccttcgagcg	ctacatggcc	240
cagctcaaat	gtactactt	tgattacaan	gagcagctcc	ccgagtcagc	ctatatgcac	300
cagctcttgg	gcctcaacct	cctcttcttg	ctgtcccaga	accgggtggc	tgantnccac	360
acgganttgg	ancggctgcc	tgcccaanga	catacanacc	aatgtctaca	tcnaccacca	420
gtgtcctgga	gcaatactga	tgganggcag	ctaccncaaa	gtnttctctg	ccnagggtaa	480
catccccgcg	cgagagctac	accttcttca	ttgacatcct	gctcgacact	atcaggggatg	540
aaaatcgcn	ggttgctcca	gaaaggctnc	aanaanatcc	ttttcctga	aggcccccg	600
atncnctagt	nctagaatcg	gcccgccatc	gcggtgganc	ctccaacctt	tcgttncctt	660
ttactgaggg	tttattggcg	cccttggcgt	tatcatggtc	acncngttn	cctgtgttga	720
aattnttaac	ccccacaaat	tccacgcena	cattng			756

<210> 35

<211> 834

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(834)

<223> n = A,T,C or G

<400> 35

ggggatctct	anatnacct	gnatgcatgg	ttgtcggtgt	ggtcgctgtc	gatgaanatg	60
aacaggatct	tgcccttgaa	gctctcggct	gctgtnttta	agttgtcag	tctgccgtca	120
tagtcagaca	cnctcttggg	caaaaaacan	caggatntga	gtcttgattt	cacctccaat	180
aatcttcngg	gctgtctgct	cggtgaactc	gatgacnang	ggcagctggt	tgtgtntgat	240
aaantccanc	angttctcct	tggtgacctc	cccttcaaa	ttgttccggc	cttcatcaaa	300
cttctnnaan	angannancc	canctttgtc	gagctggnat	ttgganaaca	cgctactgtt	360
ggaaactgat	cccaaagtgt	atgtcatcca	tcgcctctgc	tgcttgcaaa	aaacttgctt	420
ggcncaaate	cgactcccen	tccttgaaag	aagccnatca	cacccccctc	cctggactcc	480
nncaangact	ctnccgctnc	cccntccnng	cagggttggg	ggcannccgg	gccentgcgc	540
ttcttcagcc	agttcacnat	nttcatcagc	ccctctgcca	gctgtnttat	tccttggggg	600
ggaanccgtc	ttcccttccc	tgaannaact	ttgaccgtng	gaatagccgc	gcntcncnt	660
acntnctggg	ccgggttcaa	antccctccn	ttgncnntcn	cctcgggcca	ttctggattt	720
nccnaacttt	ttccttcccc	cnccccnccg	ngtttggntt	tttcatnggg	ccccaaactct	780

gctnttggcc antcccttgg gggcntntan cccccctnt ggtcccntng ggcc 834

<210> 36
 <211> 814
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1) ... (814)
 <223> n = A,T,C or G

<400> 36
 cggncgcttt cngcgcgc cccgtttcca tgacnaaggc tcccttcang ttaaatacnn 60
 cctagnaaac attaatgggt tgctctacta atacatcata cnaaccagta agcctgcca 120
 naacgccaac tcaggccatt cctaccaaag gaagaaaggc tggctctctcc acccctgta 180
 ggaaaggcct gccttgtaag acaccacaat ncggctgaat ctnaagtctt gtgttttact 240
 aatggaaaaa aaaaataaac aanaggtttt gttctcatgg ctgcccaccg cagcctggca 300
 ctaaaacanc ccagcgctca cttctgcttg ganaaatatt ctttgctctt ttggacatca 360
 ggcttgatgg tatcactgcc acntttccac ccagctgggc ncccttcccc catntttgtc 420
 antganctgg aaggcctgaa ncttagtctc caaaagtctc ngcccacaag accggccacc 480
 aggggangtc ntttncagtg gatctgccaa anantaccn tatcatcnnt gaataaaaag 540
 gccctgaac ganatgcttc cancancctt taagacccat aatcctngaa ccatggtgcc 600
 ctccgggtct gatccnaaag gaatgttctt ggggtccant cctcctttg ttnccttacgt 660
 tgtnttggac centgctn gn atnaccaan tganatcccc ngaagcacc tnccttggc 720
 atttganttt cntaaattct ctgccctacn nctgaaagca cnattccctn ggcnccnaan 780
 ggngaactca agaaggtctn ngaaaaacca cncn 814

<210> 37
 <211> 760
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1) ... (760)
 <223> n = A,T,C or G

<400> 37
 gcatgtgct ctctctcaaa gttgttcttg ttgccataac aaccaccata ggtaaaagcg 60
 gcgcagtgtt cgctgaagg gttgtagtac cagcgcggga tgctctcctt gcagagtcct 120
 gtgtctggca ggtccacgca atgccctttg tcaactggga aatggatgag ctggagctcg 180
 tcnaanccac tcgtgtattt ttcacangca gcctctccg aagcntccg gcagttgggg 240
 gtgtcgtcac actccactaa actgtcgatn cancagccca ttgctgcagc ggaactgggt 300
 gggctgacag gtgccagaac aactggatn ggctttcca tggaaaggcc tgggggaaat 360
 cncctnancc caaactgcct ctcaaaggcc accttgaca ccccgacagg ctagaaatgc 420
 actctctctt ccaaaggtag ttgttcttgt tgcccaagca ncctccanca aaccaaanc 480
 ttgcaaaatc tgctccgtgg gggatcatnnn taccanggtt ggggaaanaa acccggcngn 540
 gancncctt gtttgaatgc naaggnaata atcctcctgt cttgcttggg tggaaagca 600
 caattgaact gttaacnttg ggccnggtc cncntgggtg gtctgaaact aatcaccgtc 660
 actggaaaaa ggtangtgcc ttccttgaat tcccaaant cccctngntt tgggtnttt 720
 ctctctncc ctaaaaatcg tnttcccccc cntanggcg 760

<210> 38
 <211> 724
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(724)
 <223> n = A,T,C or G

<400> 38
 tttttttttt tttttttttt tttttttttt ttttttaaaa cccctccat tgaatgaaaa 60
 ctccnaaat tgtccaaccc cctcnnccaa atnnccattt ccgggggggg gttccaaacc 120
 caaattaatt ttgganttta aattaaatnt tnatnngggg aanaanccaa atgtnaagaa 180
 aatttaaccc attatnaact taaatnccn gaaaccntg gnttccaaaa atttttaacc 240
 cttaaattccc tccgaaattg ntaanggaaa accaaattcn cctaaggctn tttgaagggt 300
 ngatttaaac ccccttnant tnttttnacc cnngnctnaa ntatttngnt tccggtgttt 360
 tccntttaan cntnnggtaac tcccgnataat gaannnccct aanccaatta aaccgaattt 420
 tttttgaatt ggaaattccn ngggaattna ccgggggtttt tccnttttg ggcccatncc 480
 cccnctttcg ggggttggn ntaggttgaa tttttnnang ncccaaaaaa ncccccaana 540
 aaaaaactcc caagnnttaa ttngaantnc ccccttccca ggcttttttg gaaaggnggg 600
 tttntggggg ccngggantt cnttccccn ttncncccc ccccccnggt aaanggttat 660
 ngnttttggg ttttggggcc ctnnanggac ctcccgatn gaaattaaat ccccggnccg 720
 gccg 724

<210> 39
 <211> 751
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(751)
 <223> n = A,T,C or G

<400> 39
 tttttttttt tttttctttg ctacacattta atttttattt tgattttttt taatgctgca 60
 caacacaata tttatttcat ttgtttcttt tatttcattt tatttgtttg ctgctgctgt 120
 tttatttatt tttactgaaa gtgagaggga acttttgttg ccttttttcc tttttctgta 180
 ggccgcctta agctttctaa atttggaaca tctaagcaag ctgaanggaa aaggggggtt 240
 cgcaaaatca ctccggggaa nggaaagggt gctttgttaa tcatgcccta tgggtgggtga 300
 ttaactgctt gtacaattac ntttacttt taattaattg tgctnaangc ttttaattana 360
 cttgggggtt ccttccccan accaaccncc ctgacaaaaa gtgccngccc tcaaatnatg 420
 tcccgcnnt cnttgaaaca cacngcngaa ngttctcatt ntcccnccn caggtnaaaa 480
 tgaagggtta ccatntttta cncacacct acntggcnnn gcctgaatcc tcnaaaaan 540
 cctcaannc aatnctnng ccccggtcnc gentnngtcc cncccgggt cgggaantn 600
 ccccccnnga anncnntnnc naacnaaatt ccgaaaatat tcccnntcnc tcaattcccc 660
 cnnagactnt cctcnncnan cncaattttc tttntntcac gaacnccgnc cnnaaaatgn 720
 nnnncnctc cncnngtcen naatcnccan c 751

<210> 40
 <211> 753
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(753)
 <223> n = A,T,C or G

<400> 40
 gtgggtattt ctgtaagatc aggtgttcc cctcgtagg tttagaggaa acaccctcat 60
 agatgaaac cccccgaga cagcagcact gcaactgcc aagcagccgg gtagggaggg 120

```

cgccctatgc acagctgggc ccttgagaca gcagggcttc gatgtcaggc tcgatgtcaa 180
tgggtctggaa ggcggcggtg tacctgcgta ggggcacacc gtcagggccc accaggaact 240
tctcaaagtt ccaggcaacn tcgttgcgac acaccggaga ccaggatn agcttggggt 300
cggtcataaan cgcggtggcg tcgtcgttgg gagctggcag ggcctcccgc aggaaggcna 360
ataaaaggty cgccccgca ccgttcant cgcacttctc naanaccatg angttgggct 420
cnaacccacc accannccgg acttccttga nggaattccc aaatctcttc gntcttgggc 480
ttctnctgat gccctanctg gttgcccnng atgccaanca nccccaancc ccgggggtcct 540
aaancaccn cctcctcntt tcactctgggt tntntcccc ggacntggt tcctctcaag 600
ggancccata tctcnaccan tactcacent nccccccent gnnacccanc cttctanngn 660
ttccncccg ncctctggcc cntcaaanan gcttnacna cctgggtctg ccttcccccc 720
tnccctatct gnacccnctn tttgtctcan tnt 753

```

```

<210> 41
<211> 341
<212> DNA
<213> Homo sapien

```

```

<400> 41
actatatcca tcacaacaga catgcttcat cccatagact tcttgacata gcttcaaagt 60
agtgaaccca tccttgattt atatacatat atgttctcag tattttggga gcctttccac 120
ttctttaaac cttgttcatt atgaacactg aaaataggaa tttgtgaaga gttaaaaagt 180
tatagcttgt ttacgtagta agtttttgaa gtctacattc aatccagaca cttagttag 240
tggtaaactg tgatttttaa aaaatatcat ttgagaatat tctttcagag gtattttcat 300
ttttactttt tgattaattg tgttttatat attagggtag t 341

```

```

<210> 42
<211> 101
<212> DNA
<213> Homo sapien

```

```

<400> 42
acttactgaa tttagttctg tgctcttctt tatttagtgt tgtatcataa atactttgat 60
gtttcaaaca ttctaaataa ataattttca gtggcttcat a 101

```

```

<210> 43
<211> 305
<212> DNA
<213> Homo sapien

```

```

<400> 43
acatctttgt tacagtctaa gatgtgttct taaatcacca ttccttctg gtcctcacc 60
tcagggtgg tctcacactg taattagagc tattgaggag tctttacagc aaattaagat 120
tcagatgct tgctaagtct agagttctag agttatgtt cagaaagtct aagaaacca 180
cctcttgaga ggtcagtaaa gaggacttaa tatttcatat ctacaaaatg accacaggat 240
tggtacaga acgagagtta tcctggataa ctcagagctg agtacctgcc cgggggcgc 300
tcgaa 305

```

```

<210> 44
<211> 852
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(852)
<223> n = A,T,C or G

```

```

<400> 44

```

```

acataaatat cagagaaaag tagtctttga aatattttacg tccaggaggtt ctttgtttct 60
gattatttgg tgtgtgtttt ggtttgtgtc caaagtattg gcagcttcag ttttcatttt 120
ctctccatcc tcgggcattc ttcccaaatt tatataccag tcttcgtcca tccacacgct 180
ccagaatttc tctttttag tagtatctca tagctcggct gagcttttca taggtcatgc 240
tgctgttggt cttcttttta ccccatagct gagccactgc ctctgatttc aagaacctga 300
agacgccctc agatcgggtc tcccatttta ttaatcctgg gttcttgtct gggttcaaga 360
ggatgtcgcg gatgaattcc cataagttag tccctctcgg gttgtgcttt ttggtgtggc 420
acttggcagg ggggtcttgc tcctttttca taccaggtga ctctgcaaca ggaaggtgac 480
tggtggttgt catggagatc tgagcccggc agaaagtttt gctgtccaac aaatctactg 540
tgctaccata gttggtgtca tataaatagt tctngtcttt ccagggtgtc atgatggaag 600
gctcagtttg ttcagtcttg acaatgacat tgtgtgtgga ctggaacagg tcactactgc 660
actggcggtt ccacttcaga tgctgcaagt tgctgtagag gagntgcccc gccgtccctg 720
ccgcccgggt gaactcctgc aaactcatgc tgcaaagggt ctgcccgttg atgtcgaact 780
cntggaaagg gatacaattg gcatccagct ggttgggtgc caggaggtga tggagccact 840
cccacacctg gt 852

```

```

<210> 45
<211> 234
<212> DNA
<213> Homo sapien

```

```

<400> 45
acaacagacc cttgctcgtc aacgacctca tgctcatcaa gttggaagaa tccgtgtccg 60
agtctgacac catccggagc atcagcattg cttcgcagtg ccctaccgcg gggaaactctt 120
gcctcgtttc tggctggggt ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg 180
tgaacgtgtc ggtggtgtct gaggagggtc gcagtaagct ctatgaccgc ctgt 234

```

```

<210> 46
<211> 590
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (590)
<223> n = A,T,C or G

```

```

<400> 46
actttttatt taaattgttt taaggcagat ctatgagaat gatagaaaac atggtgtgta 60
atttgatagc aatattttgg agattacaga gtttttagtaa ttaccaatta cacagttaaa 120
aagaagataa tatattccaa gcanatacaa aatatctaat gaaagatcaa ggcaggaaaa 180
tgantataac taattgacaa tggaaaatca attttaatgt gaattgcaca ttatccttta 240
aaagcttttc aaanaanaa ttattgcagt ctanttaatt caaacagtgt taaatgggtat 300
caggataaan aactgaaggg canaaagaat taattttcac ttcattgtaac ncacccanat 360
ttacaatggc ttaaatgcan ggaaaaagca gtggaagtag ggaagtantc aagggtctttc 420
tggtctctaa tctgccttac tctttgggtg tggttttgat cctctggaga cagctgccag 480
ggctcctggt atatcccaa tcccagcagc aagatgaagg gatgaaaaag gacacatgct 540
gccttccttt gaggagactt catctcactg gccaacactc agtcacatgt 590

```

```

<210> 47
<211> 774
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (774)
<223> n = A,T,C or G

```

```

<400> 47
acaagggggc ataatgaagg agtggggana gatttttaaag aaggaaaaaa aacgaggccc      60
tgaacagaat tttcctgnac aacggggcctt caaaataatt ttcttgggga gggtcaagac      120
gcttcactgc ttgaaactta aatggatgtg ggacanaatt ttctgtaatg accctgaggg      180
cattacagac gggactcttg gaggaaggat aaacagaaag gggacaaaag ctaatcccaa      240
aacatcaaag aaaggaaggt ggcgtcatat ctcccagcct acacagttct ccagggtctct      300
cctcatccct ggaggacgac agtggaggaa caactgacca tgtcccagc ctctgtgtg      360
ctggctcctg gtcttcagcc cccagctctg gaagcccacc ctctgctgat cctgcgtggc      420
ccacactcct tgaacacaca tccccaggtt atattccttg acatggctga acctcctatt      480
cctacttccg agatgccttg ctccctgcag cctgtcaaaa tcccactcac cctccaaacc      540
acggcatggg aagcctttct gacttgcttg attactccag catcttggaa caatccctga      600
ttcccactc cttagaggca agatagggtg gttaagagta gggctggacc acttgagcc      660
aggtctgttg cttcaaattn tggctcattt acgagctatg ggaccttggg caagtnatct      720
tcacttctat gggcntcatt ttgttctacc tgcaaaatgg gggataataa tagt          774

```

```

<210> 48
<211> 124
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (124)
<223> n = A,T,C or G

```

```

<400> 48
canaaattga aattttataa aaaggcattt ttctcttata tccataaaat gatataattt      60
ttgcaantat anaaatgtgt cataaattat aatgttcctt aattacagct caacgcaact      120
tggt                                              124

```

```

<210> 49
<211> 147
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (147)
<223> n = A,T,C or G

```

```

<400> 49
gccgatgcta ctattttatt gcaggagggtg ggggtgtttt tattattctc tcaacagctt      60
tgtggctaca ggtgggtgtct gactgcatna aaaanttttt tacgggtgat tgcaaaaatt      120
ttagggcacc catatcccaa gcantgt                    147

```

```

<210> 50
<211> 107
<212> DNA
<213> Homo sapien

```

```

<400> 50
acattaaatt aataaaagga ctgttgggggt tctgctaaaa cacatgggctt gatatatgtc      60
atggtttgag gttaggagga gttaggcata tgttttggga gaggggt                    107

```

```

<210> 51
<211> 204
<212> DNA

```

<213> Homo sapien

<400> 51

gtcctaggaa	gtctagggga	cacacgactc	tgggggtcacg	gggccgacac	acttgacagg	60
cggaagaa	aggcagagaa	gtgacaccgt	cagggggaaa	tgacagaaag	gaaaatcaag	120
gccttgcaag	gtcagaaagg	ggactcaggg	cttccaccac	agccctgccc	cacttggcca	180
cctccctttt	gggaccagca	atgt				204

<210> 52

<211> 491

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (491)

<223> n = A,T,C or G

<400> 52

acaagataa	catttatctt	ataacaaaaa	tttgatagtt	ttaaaggtta	gtattgtgta	60
gggtattttt	caaaagacta	aagagataac	tcaggtaaaa	agttagaaat	gtataaaaaca	120
ccatcagaca	ggttttttaa	aaacaacata	ttacaaaatt	agacaatcat	ccttaaaaaa	180
aaaacttctt	gtatcaattt	cttttgttca	aaatgactga	cttaantatt	tttaaataatt	240
tcanaaacac	ttcctcaaaa	attttcaana	tggtagcttt	canatgtnc	ctcagtccca	300
atgttgctca	gataaataaa	tctcgtgaga	acttaccacc	caccacaagc	tttctggggc	360
atgcaacagt	gtcttttctt	tnctttttct	tttttttttt	ttacaggcac	agaaactcat	420
caattttatt	tgataacaa	agggctctcca	aatttatattg	aaaaataaat	ccaagttaat	480
atcactcttg	t					491

<210> 53

<211> 484

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (484)

<223> n = A,T,C or G

<400> 53

acataattta	gcagggctaa	ttaccataag	atgctattta	ttaanaggtn	tatgatctga	60
gtattaacag	ttgctgaagt	ttggattttt	tatgcagcat	tttctttttg	ctttgataac	120
actacagAAC	ccttaaggac	actgaaaatt	agtaagttaa	gttcagaaac	attagctgct	180
caatcaaatt	tctacataac	actatagtaa	ttaaaacggt	aaaaaaaaag	gttgaaattct	240
gcactagtat	anaccgctcc	tgtcaggata	anactgcttt	ggaacagaaa	gggaaaaanc	300
agctttgant	ttctttgtgc	tgatangagg	aaaggctgaa	ttaccttggt	gcctctccct	360
aatgattggc	aggctcngta	aatnccaaaa	catattccaa	ctcaacactt	cttttcncng	420
tancttgant	ctgtgtattc	caggancagg	cggatggaat	gggccagccc	ncggatgttc	480
cant						484

<210> 54

<211> 151

<212> DNA

<213> Homo sapien

<400> 54

actaaacctc	gtgcttggtga	actccataca	gaaaacggtg	ccatccctga	acacggctgg	60
ccactgggta	tactgctgac	aaccgcaaca	acaaaaaacac	aaatccttgg	cactggctag	120

tctatgtcct ctcaagtgcc tttttgtttg t 151

<210> 55
 <211> 91
 <212> DNA
 <213> Homo sapien

<400> 55
 acctggcttg tctccgggtg gttcccggcg cccccacgg tccccagaac ggacactttc 60
 gccctccagt ggatactcga gccaaagtgg t 91

<210> 56
 <211> 133
 <212> DNA
 <213> Homo sapien

<400> 56
 ggcggatgtg cgttggttat atacaaatat gtcattttat gtaagggact tgagtatact 60
 tggatttttg gtatctgtgg gttgggggga cgggccagga accaatacc catggatacc 120
 aagggacaac tgt 133

<210> 57
 <211> 147
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(147)
 <223> n = A,T,C or G

<400> 57
 actctggaga acctgagccg ctgctccgcc tctgggatga ggtgatgcan gcngtggcgc 60
 gactgggagc tgagcccttc cctttgcgcc tgcctcagag gattgttgcc gacntgcana 120
 tctcantggg ctggatncat gcagggt 147

<210> 58
 <211> 198
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(198)
 <223> n = A,T,C or G

<400> 58
 acagggatat aggtttnaag ttattgtnat tgtaaaatac attgaatddd ctgtatactc 60
 tgattacata catttatcct ttaaaaaaga tgtaaattctt aatttttatg ccacttatta 120
 atttaccaat gagttacctt gtaaatgaga agtcatgata gcaactgaatt ttaactagtt 180
 ttgacttcta agtttgggt 198

<210> 59
 <211> 330
 <212> DNA
 <213> Homo sapien

<400> 59

acaacaaatg ggttgtagagg aagtccttacc agcaaaactg gtgatggcta ctgaaaagat	60
ccattgaaaa ttatcattaa tgatttttaa tgacaagtta tcaaaaactc actcaatttt	120
cacctgtgct agcttgctaa aatgggaggt aactctagag caaatatagt atcttctgaa	180
tacagtcaat aaatgacaaa gccagggcct acagggtggt tccagacttt ccagacccag	240
cagaaggaaat ctattttacc acatggatct ccgtctgtgc tcaaaatacc taatgatatt	300
tttcgtcttt attggacttc tttgaagagt	330

<210> 60

<211> 175

<212> DNA

<213> Homo sapien

<400> 60

accgtgggtg ccttctacat tcctgacggc tccttcacca acatctgggt ctacttcggc	60
gtcgtgggtc ccttcctctt catcctcacc cagctgggtc tgctcatcga ctttgcgcac	120
tcctggaacc agcgtgggtc gggcaaggcc gaggagtgcg attcccgtgc ctggt	175

<210> 61

<211> 154

<212> DNA

<213> Homo sapien

<400> 61

acccacttt tcctcctgtg agcagtctgg acttctcact gctacatgat gagggtagt	60
ggttggtgct cttcaacagt atcctccctt ttccggatct gctgagccgg acagcagtgc	120
tggactgcac agccccgggg ctccacattg ctgt	154

<210> 62

<211> 30

<212> DNA

<213> Homo sapien

<400> 62

cgctcgagcc ctatagtgag tcgtattaga	30
----------------------------------	----

<210> 63

<211> 89

<212> DNA

<213> Homo sapien

<400> 63

acaagtcatt tcagcaccct ttgctcttca aaactgacca tcttttatat ttaatgcttc	60
ctgtatgaat aaaaatgggt atgtcaagt	89

<210> 64

<211> 97

<212> DNA

<213> Homo sapien

<400> 64

accggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa ggttctgcag	60
aatcagtgc tccaggattg gtccttggat ctgggggt	97

<210> 65

<211> 377

<212> DNA

<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(377)
 <223> n = A,T,C or G

<400> 65
 acaacaanaa ntcccttctt taggccactg atggaaacct ggaacccctt ttgatggca 60
 gcatggcgctc ctaggccttg acacagcggc tggggtttgg gctntcccaa accgcacacc 120
 ccaaccctgg tctaccaca nttctggcta tgggctgtct ctgccactga acatcagggt 180
 tcggtcataa natgaaatcc caanggggac agaggtcagt agagggaagct caatgagaaa 240
 ggtgctgttt gctcagccag aaaacagctg cctggcattc gccgctgaac tatgaacccg 300
 tgggggtgaa ctaccccccag gaggaatcat gcctgggcga tgcaanggtg ccaacaggag 360
 gggcgggagg agcatgt 377

<210> 66
 <211> 305
 <212> DNA
 <213> Homo sapien

<400> 66
 acgcctttcc ctacagaattc agggaagaga ctgtcgctg ccttcctccg ttgttgctg 60
 agaaccctgt tgccccttcc caccatatcc accctcgctc catctttgaa ctcaaacacg 120
 aggaactaac tgcaccctgg tctctcccc agtccccagt tcaccctcca tccctcacct 180
 tcttccactc taagggatat caacactgcc cagcacaggg gccctgaatt tatgtggttt 240
 ttatatattt ttttaataaga tgcactttat gtcatttttt aataaagtct gaagaattac 300
 tgttt 305

<210> 67
 <211> 385
 <212> DNA
 <213> Homo sapien

<400> 67
 actacacaca ctccacttgc ctttgtgaga cactttgtcc cagcacttta ggaatgctga 60
 ggtcggacca gccacatctc atgtgcaaga ttgccagca gacatcagggt ctgagagttc 120
 cccttttaaa aaaggggact tgcttaaaaa agaagtctag ccacgattgt gtagagcagc 180
 tgtgctgtgc tggagattca cttttgagag agttctctc tgagacctga tctttagagg 240
 ctgggcagtc ttgcacatga gatggggctg gtctgatctc agcactcctt agtctgcttg 300
 cctctccag gcccccagcc tggccacacc tgcttacagg gcactctcag atgccatac 360
 catagtttct gtgctagtgg accgt 385

<210> 68
 <211> 73
 <212> DNA
 <213> Homo sapien

<400> 68
 acttaaccag atatattttt accccagatg gggatattct ttgtaaaaaa tgaaaataaa 60
 gtttttttaa tgg 73

<210> 69
 <211> 536
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(536)

<223> n = A,T,C or G

<400> 69

actagtccag	tgtggtggaa	ttccattgtg	ttgggggctc	tcaccctcct	ctcctgcagc	60
tccagctttg	tgctctgcct	ctgaggagac	catggcccag	catctgagta	ccctgctgct	120
cctgctggcc	accctagctg	tggccctggc	ctggagcccc	aaggaggagg	ataggataat	180
cccggtggc	atctataacg	cagacctcaa	tgatgagtgg	gtacagcgtg	cccttcactt	240
cgccatcagc	gagtataaca	aggccaccaa	agatgactac	tacagacgtc	cgctgcgggt	300
actaagagcc	aggcaacaga	ccgttggggg	ggtgaattac	ttcttcgacg	tagaggtggg	360
ccgaaccata	tgtaccaagt	cccagcccaa	cttggacacc	tgtgccttcc	atgaacagcc	420
agaactgcag	aagaaacagt	tgtgctcttt	cgagatctac	gaagttccct	ggggagaaca	480
gaangtccct	gggtgaaatc	caggtgtcaa	gaaatcctan	ggatctgttg	ccaggc	536

<210> 70

<211> 477

<212> DNA

<213> Homo sapien

<400> 70

atgacccta	acaggggccc	tctcagccct	cctaatagacc	tccggcctag	ccatgtgatt	60
tcacttccac	tccataacgc	tctcatact	aggcctaata	accaacacac	taaccatata	120
ccaatgatgg	cgcgatgtaa	cacgagaaag	cacataccaa	ggccaccaca	caccacctgt	180
ccaaaaaggc	cttcgatacg	ggataatcct	atattattacc	tcagaagttt	ttttcttcgc	240
agggattttt	ctgagccttt	taccactcca	gcctagcccc	taccccccaa	ctaggagggc	300
actggccccc	aacaggcatc	accccgttaa	atcccctaga	agtccactc	ctaaacacat	360
ccgtattact	cgcacagga	gtatcaatca	cctgagctca	ccatagtcta	atagaaaaca	420
accgaaacca	aattattcaa	agcactgctt	attacaattt	tactgggtct	ctatttt	477

<210> 71

<211> 533

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(533)

<223> n = A,T,C or G

<400> 71

agagctatag	gtacagtgtg	atctcagctt	tgcaaacaca	ttttctacat	agatagtact	60
aggattaat	agatatgtaa	agaaagaaat	cacaccatta	ataatggtaa	gattgggtta	120
tgtgatttta	gtggattttt	tggcaccctt	atatatgttt	tccaaacttt	cagcagtgat	180
attattttcca	taacttaaaa	agtgagtttg	aaaaagaaaa	tctccagcaa	gcatctcatt	240
taaataaagg	tttgtcatct	ttaaaaatac	agcaatatgt	gactttttta	aaaagctgtc	300
aaatagggtg	gaccctacta	ataattatta	gaaatacatt	taaaaacatc	gagtacctca	360
agtcagtttg	ccttgaaaaa	tatcaaatat	aactcttaga	gaaatgtaca	taaaagaatg	420
cttcgtaatt	ttggagtang	aggttccctc	ctcaattttg	tattttttaa	aagtacatgg	480
taaaaaaaaa	aattcacaac	agtatataag	gctgtaaaat	gaagaattct	gcc	533

<210> 72

<211> 511

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(511)

<223> n = A,T,C or G

```

<400> 72
tattacggaa aaacacacca cataattcaa ctancaaaga anactgcttc agggcgtgta      60
aaatgaaagg ctccaggca gttatctgat taaagaacac taaaagaggg acaaggctaa      120
aagccgcagg atgtctacac tatancaggc gctatttggg ttggctggag gagctgtgga      180
aaacatggan agattgggtgc tgganatcgc cgtggctatt cctcattgtt attacanagt      240
gaggttctct gtgtgcccac tggtttgaaa accgttctnc aataatgata gaatagtaca      300
cacatgagaa ctgaaatggc ccaaaccag aaagaaagcc caactagatc ctcagaanac      360
gcttctaggg acaataaccg atgaagaaa gatggcctcc ttgtgcccc gtctgttatg      420
atttctctcc attgcagcna naaaccggtt cttctaagca aacncagggtg atgatggcna      480
aaatacaccc cctcttgaag naccnggagg a                                     511

```

```

<210> 73
<211> 499
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (499)
<223> n = A,T,C or G

```

```

<400> 73
cagtgccagc actggtgccca gtaccagtac caataacagt gccagtgccca gtgccagcac      60
cagtgggtggc ttcagtgcct gtgccagcct gaccgccact ctcacatttg ggctcttcgc      120
tggccttggg ggagctgggt ccagcaccag tggcagctct ggtgcctgtg gtttctccta      180
caagtgagat tttagatatt gttaatcctg ccagtcttct tcttcaagcc aggggtgcac      240
ctcagaaacc tactcaacac agcactctag gcagccacta tcaatcaatt gaagttgaca      300
ctctgcatta aatctatttg ccatttctga aaaaaaaaaa aaaaaaaggg cggccgctcg      360
antctagagg gcccgtttaa acccgctgat cagcctcgac tgtgccttct anttgccagc      420
catctgttgt ttgcccctcc cccgntgcct tccttgaccc tggaaaagtgc cactcccact      480
gtcctttcct aantaaat                                     499

```

```

<210> 74
<211> 537
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (537)
<223> n = A,T,C or G

```

```

<400> 74
tttcatagga gaacacactg aggagatact tgaagaatth ggattcagcc gcgaagagat      60
ttatcagctt aactcagata aaatcattga aagtaataag gtaaaagcta gtctctaact      120
tccaggccca cggctcaagt gaatttgaat actgcattta cagtgtagag taacacataa      180
cattgtatgc atggaaacat ggaggaaacag tattacagtg tcctaccact ctaatcaaga      240
aaagaattac agactctgat tctacagtga tgattgaatt ctaaaaatgg taatcattag      300
ggcttttgat ttataanact ttgggtactt atactaaatt atggtagtta tactgccttc      360
cagtttgctt gatataattg ttgatattaa gattcttgac ttatattttg aatgggttct      420
actgaaaaan gaatgatata ttcttgaaga catcgatata catttattta cactcttgat      480
tctacaatgt agaaaatgaa ggaaatgccc caaattgtat ggtgataaaa gtcccgt      537

```

```

<210> 75
<211> 467
<212> DNA
<213> Homo sapien

```

<220>
 <221> misc_feature
 <222> (1)...(467)
 <223> n = A,T,C or G

<400> 75
 caaanacaat tgttcaaaag atgcaaatga tacactactg ctgcagctca caaacacctc 60
 tgcataattac acgtacctcc tcctgtctcct caagtagtgt ggtctatatt gccatcatca 120
 cctgtctgtct gcttagaaga acggctttct gctgcaangg agagaaatca taacagacgg 180
 tggcacaagg aggccatctt ttctctcatcg gttattgtcc ctagaagcgt cttctgagga 240
 tctagtggg ctttctttct gggtttgggc catttcantt ctcatgtgtg tactattcta 300
 tcattattgt ataacgggtt tcaaaccngt gggcacncag agaacctcac tctgtaataa 360
 caatgaggaa tagccacggg gatctccagc accaaatctc tccatgttnt tccagagctc 420
 ctccagccaa cccaaatagc cgctgctatn gtgtagaaca tccctgn 467

<210> 76
 <211> 400
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(400)
 <223> n = A,T,C or G

<400> 76
 aagctgacag cattcgggcc gagatgtctc gctccgtggc cttagctgtg ctgcgcctac 60
 tctctctttc tggcctggag gctatccagc gtactccaaa gattcagggt tactcacgtc 120
 atccagcaga gaatggaaag tcaaatttcc tgaattgcta tgtgtctggg tttcatccat 180
 ccgacattga agttgactta ctgaagaatg gagagagaat tgaaaaagtg gagcattcag 240
 acttgtcttt cagcaaggac tggctctttc atctcttgta ctacactgaa ttcaccccca 300
 ctgaaaaaga tgagtatgcc tgccgtgtga accatgtgac tttgtcacag cccaagatng 360
 ttnagtggga tcganacatg taagcagcan catgggaggt 400

<210> 77
 <211> 248
 <212> DNA
 <213> Homo sapien

<400> 77
 ctggagtggc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcacct 60
 ccagctgccc cggcggggga tgcgaggctc ggagcaccct tgcccggctg tgattgctgc 120
 caggcaactgt tcatctcagc ttttctgtcc ctttgtctcc ggcaagcgt tctgtgaaa 180
 gttcatatct ggagcctgat gtcttaacga ataaaggctc catgctccac ccgaaaaaaa 240
 aaaaaaaa 248

<210> 78
 <211> 201
 <212> DNA
 <213> Homo sapien

<400> 78
 actagtccag tgttggtggaa ttccattgtg ttgggcccac cacaatggct acctttaaca 60
 tcacccagac cccgccctgc ccgtgcccac cgctgctgct aacgacagta tgatgcttac 120
 tctgtctact ggaaactatt tttatgtaat taatgtatgc tttcttgttt ataaatgcct 180
 gattttaaaaa aaaaaaaaaa a 201

<210> 79
 <211> 552
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(552)
 <223> n = A,T,C or G

<400> 79
 tccttttgtt aggtttttga gacaacccta gacctaaact gtgtcacaga cttctgaatg 60
 tttaggcagt gctagtaatt tcctcgtaat gattctgtta ttactttcct attctttatt 120
 cctctttctt ctgaagatta atgaagttga aaattgaggt ggataaatac aaaaaggtag 180
 tgtgatagta taagtatcta agtgcagatg aaagtgtgtt atatatatcc attcaaaatt 240
 atgcaagtta gtaattactc agggttaact aaattacttt aatatgctgt tgaacctact 300
 ctgttccttg gctagaaaaa attataaaca ggactttgtt agtttgggaa gccaaattga 360
 taatattcta tgttctaaaa gttgggctat acataaanta tnaagaaata tggaaatttta 420
 ttcccaggaa tatgggggtc atttatgaat antaccggg anagaagttt tgantnaaac 480
 cngttttggt taatacgta atagtctctn aatnaacaag gcntgactta tttccaaaaa 540
 aaaaaaaaaa aa 552

<210> 80
 <211> 476
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(476)
 <223> n = A,T,C or G

<400> 80
 acagggattt gagatgctaa ggccccagag atcgtttgat ccaacctctt tattttcaga 60
 ggggaaaaatg gggcctagaa gttacagagc atctagctgg tgcgctggca cccctggcct 120
 cacacagact cccgagtagc tgggactaca ggacacagct cactgaagca ggccctgttt 180
 gcaattcacg ttgccacctc caacttaaac attcttcata tgtgatgtcc ttagtcacta 240
 aggttaaaact ttcccaccca gaaaaggcaa cttagataaa atcttagagt actttcatac 300
 tcttctaagt cctcttccag cctcactttg agtcctcctt gggggttgat aggaantntc 360
 tcttggtttt ctcaataaaa tctctatcca tctcatgttt aatttggtac gcntaaaaat 420
 gctgaaaaaa ttaaatgtgt ctggtttcnc tttaaaaaaa aaaaaaaaaa aaaaaa 476

<210> 81
 <211> 232
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(232)
 <223> n = A,T,C or G

<400> 81
 tttttttttg tatgcntcn ctgtggngtt attgttgctg ccacctgga ggagcccagt 60
 ttctttctgta tctttctttt ctgggggagc ttcttggtc tgccctcca ttcccagcct 120
 ctcatcccca tcttgcaact ttgctagggg tggaggcgct ttcttggtag cccctcagag 180
 actcagtcag cgggaataag tcctaggggt ggggggtgtg gcaagccggc ct 232

<210> 82
 <211> 383
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (383)
 <223> n = A,T,C or G

<400> 82
 aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactggtgcc 60
 agtaccagta ccaataacat gccagtgcc gtgccagcac cagtgggtggc ttcagtgctg 120
 gtgccagcct gaccgccact ctcacatttg ggctcttcgc tggccttggg ggagctgggtg 180
 ccagcaccag tggcagctct ggtgcctgtg gttctccta caagtgaat ttagatatt 240
 gttaatcctg ccagtctttc tcttcaagcc aggggtgcac ctcagaaacc tactcaacac 300
 agcactctng gcagccacta tcaatcaatt gaagttgaca ctctgcatta aatctatttg 360
 ccatttcaaa aaaaaaaaaaaa aaa 383

<210> 83
 <211> 494
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (494)
 <223> n = A,T,C or G

<400> 83
 accgaattgg gaccgctggc ttataagcga tcatgtcctc cagtattacc tcaacgagca 60
 gggagatcga gtctatacgc tgaagaaatt tgaccgatg ggacaacaga cctgctcagc 120
 ccatacctgct cgggttctccc cagatgacaa atactctcga caccgaatca ccatcaagaa 180
 acgcttcaag gtgctcatga cccagcaacc gcgccctgtc ctctgagggg ccttaaactg 240
 atgtcttttc tgccaactgt taccctctcg agactcctga accaaactct tcggactgtg 300
 agccctgatg cctttttggc agccatactc tttggcctcc agtctctcgt ggcgattgat 360
 tatgcttggtg tgaggcaatc atggtggcat caccatnaa gggaacacat ttganttttt 420
 tttcncatat tttaaattac naccagaata ntccagaata aatgaattga aaaactctta 480
 aaaaaaaaaa aaaa 494

<210> 84
 <211> 380
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (380)
 <223> n = A,T,C or G

<400> 84
 gctggtagcc tatggcgtgg ccacggangg gctcctgagg caccgggacag tgacttccca 60
 agtatcctgc gccgcgtctt ctaccgtccc tacctgcaga tcttcgggca gattcccag 120
 gaggacatgg acgtggccct catggagcac agcaactgct cgtcggagcc cggcttcttg 180
 gcacaccctc ctggggccca ggcgggcacc tgcgtctccc agtatgccaa ctggctgggtg 240
 gtgctgctcc tcgtcatctt cctgctcgtg gccaacatcc tgctggtcac ttgctcattg 300
 ccatgttcag ttacacattc ggcaaagtac agggcaacag cnatctctac tgggaaggcc 360
 agcgttnccg cctcatccgg 380

<210> 85
 <211> 481
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(481)
 <223> n = A,T,C or G

```

<400> 85
gagttagctc ctccacaacc ttgatgaggt cgtctgcagt ggcctctcgc ttcataccgc      60
tnccatcgtc atactgtagg tttgccacca cctcctgcat cttggggcgg ctaatatcca      120
ggaaactctc aatcaagtca ccgtcnatna aacctgtggc tggttctgtc ttccgctcgg      180
tgtgaaagga tctccagaag gagtgtctga tcttccccac acttttctgt actttattga      240
gtcgattctg catgtccagc aggaggttgt accagctctc tgacagtgag gtcaccagcc      300
ctatcatgcc nttgaacgtg ccgaagaaca ccgagccttg tgtggggggg gnagtctcac      360
ccagattctg cattaccaga naggcgtggc aaaaganatt gacaactcgc ccaggngaa      420
aaagaacacc tcttgggaagt gctngccgct cctcgtccnt tgggtggngc gentnccttt      480
t                                                                                   481

```

<210> 86
 <211> 472
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(472)
 <223> n = A,T,C or G

```

<400> 86
aacatcttcc tgtataatgc tgtgtaatat cgatccgatn ttgtctgctg agaattcatt      60
acttggaaaa gcaacttnaa gcctggacac tggattataa attcacaata tgcaacactt      120
taaacagtgt gtcaatctgc tcccttactt tgtcatcacc agtctgggaa taagggtatg      180
ccctattcac acctgttaaa agggcgctaa gcatttttga ttcaacatct ttttttttga      240
cacaagtccg aaaaaagcaa aagtaaacag ttnttaattt gttagccaat tcactttctt      300
catgggacag agccatttga tttaaaaagc aaattgcata atattgagct ttgggagctg      360
atatntgagc ggaagantag cttttctact tcaccagaca caactccttt catattggga      420
tgttnacnaa agttatgtct cttacagatg ggatgctttt gtggcaattc tg                   472

```

<210> 87
 <211> 413
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(413)
 <223> n = A,T,C or G

```

<400> 87
agaaaccagt atctctnaaa acaacctctc ataccttggt gacctaatth tgtgtgcgtg      60
tgtgtgtgcg cgcataattat atagacaggc acatcttttt tactttttgta aaagcttatg      120
cctcttttgg atctatatct gtgaaagttt taatgatctg ccataatgtc ttggggacct      180
ttgtcttctg tgtaaattgg actagagaaa acacctatnt tatgagtcaa tctagttngt      240
tttattcgac atgaaggaaa tttccagatn acaacactna caaactctcc cttgactagg      300

```



```

ggggacaaag aaaagcanaa ctgaacatna gaaacaattn cctgggtgaga aattncataa 360
acagaaattg ggngtatat tgaaanang catcattnaa acgttttttt ttt 413

```

```

<210> 88
<211> 448
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(448)
<223> n = A,T,C or G

```

```

<400> 88
cgcagcgggt cctctctatc tagctccagc ctctcgctg ccccaactccc cgcgtcccg 60
gtcctagccn accatggccg ggccctgctg cgcctcgctg ccatcctggc 120
cgtggccctg gccgtgagcc ccgcgcccg ctcagctccc ggcaagccgc cgcgctggt 180
gggaggccca tggaccccg gtggaagaag aaggtgtgctg gcgtgcactg gactttgccg 240
tcggnanta caacaaacc gcaacnactt ttaccnagcn cgcgtgcag gttgtgccgc 300
cccaancaaa ttgttactng gggtaantaa ttcttgaag ttgaacctgg gccaaacnng 360
tttaccagaa ccnagccaat tngaacaatt nccctccat aacagcccct tttaaaaagg 420
gaancantec tgntcttttc caaat ttt 448

```

```

<210> 89
<211> 463
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(463)
<223> n = A,T,C or G

```

```

<400> 89
gaattttgtg cactggccac tgtgatggaa ccattgggccc aggatgcttt gagtttatca 60
gtagtgtatc tgccaaagtt ggtgtgtgtaa catgagtatg taaaatgtca aaaaatttagc 120
agaggtctag gtctgcatat cagcagacag ttgtgctgtg tattttgtag ccttgaagtt 180
ctcagtgcac agttnnttct gatgcgaagt tctnattcca gtgttttagt cctttgcac 240
tttnatgtn agacttgctt ctnnaaatt gctttgtnt tctgcaggta ctatctgtgg 300
ttaacaaaa tagaannact tctctgcttn gaanatttga atatcttaca tctnaaaatn 360
aattctctcc ccatannaaa acccangccc ttggganaat ttgaaaaang gntccttcnn 420
aatcnnana anttcagntn tcatacaaca naacngganc ccc 463

```

```

<210> 90
<211> 400
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(400)
<223> n = A,T,C or G

```

```

<400> 90
agggattgaa ggtctntnt actgtcggac tgttcancca ccaactctac aagttgctgt 60
cttcactca ctgtctgtaa gcntnttaac ccagactgta tcttcataaa tagaacaat 120
tcttcaccag tcacatcttc taggaccttt ttggattcag ttagtataag ctcttcact 180
tcctttgtta agacttcac tcgtaaagtc ttaagttttg tagaaaggaa ttaattgct 240

```

cgttctctaa caatgtcctc tccttgaagt atttggtga acaaccacc tnaagtcct	300
ttgtgcatcc attttaata tacttaatag ggcattggtg cactagggtta aattctgcaa	360
gagtcacatctg tctgcaaaag ttgcgttagt atatctgcc	400

<210> 91

<211> 480

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(480)

<223> n = A,T,C or G

<400> 91

gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact	60
ggctctacccc acatgggagc agcatgccgt agntatataa ggctattccc tgagtcagac	120
atgcctcttt gactaccgtg tgccagtgtt ggtgattctc acacacctcc nncgctctt	180
tgtggaaaaa ctggcacttg nctggaacta gcaagacatc acttataaat tcaccacga	240
gacacttgaa aggtgtaaca aagcgactct tgcattgctt tttgtccctc cggcaccagt	300
tgtcaatact aaccgcgtgg tttgcctcca tcacatttgt gatctgtagc tctggataca	360
tctctgaca gtactgaaga acttcttctt ttgtttcaaa agcaactctt ggtgcctgtt	420
ngatcagggt cccatttccc agtccgaatg ttcacatggc atatnttact tcccacaaaa	480

<210> 92

<211> 477

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(477)

<223> n = A,T,C or G

<400> 92

atacagccca natcccacca cgaagatgcg cttgttgact gagaacctga tgcggctcact	60
ggtcccgtg tagccccagc gactctccac ctgctggaag cggttgatgc tgcactcctt	120
cccacgcagg cagcagcggg gccgggtcaat gaactccact cgtggcttgg gggtgacgtt	180
taantgcagg aagaggctga ccacctcgcg gtccaccagg atgcccagact gtgcgggacc	240
tgcagcgaaa ctctcgatg gtcattgagc ggaagcgaat gangcccagg gccttgccca	300
gaaccttccg cctgttctct ggcgtcacct gcagctgctg ccgctnacac tcggcctcgg	360
accagcggac aaacggcggt gaacagccgc acctcacgga tgcccantgt gtcgcgtcc	420
aggaacggcn ccagcgtgtc caggtcaatg tcggtgaanc ctccgcgggt aatggcg	477

<210> 93

<211> 377

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(377)

<223> n = A,T,C or G

<400> 93

gaacggctgg accttgctc gcattgtgct gctggcagga ataccttggc aagcagctcc	60
agtccgagca gccccagacc gctgccgccc gaagctaaag ctgcctctgg ccttcccctc	120
cgctcaatg cagaaccant agtgggagca ctgtgtttag agttaagagt gaacactgtn	180

```

tgattttact tgggaatttc ctctgttata tagcttttcc caatgctaata ttccaaacaa 240
caacaacaaa ataacatggt tgctgtttna gttgtataaa agtangtgat tctgtatnta 300
aagaaaatat tactgttaca tatactgctt gcaantttctg tattttattgg tntctctggaa 360
ataaatatat tattaata 377

```

```

<210> 94
<211> 495
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(495)
<223> n = A,T,C or G

```

```

<400> 94
ccctttgagg ggtaggggtc cagttcccag tggagaagaa aggccaggag aantgcgtgc 60
cgagctgang cagatttccc acagtgaccc cagagccctg ggctatagtc tctgacccct 120
ccaaggaaa accaccttct ggggacatgg gctggagggc aggacctaga ggcaccaagg 180
gaaggcccca ttccggggtc gtcccccgag gaggaaggga aggggctctg tgtgcccccc 240
acgaggaana ggccctgant cctgggatca nacacccctt cacgtgtatc cccacacaaa 300
tgcaagctca ccaaggtccc ctctcagtc ctccctaca ccctgaacgg nactggccc 360
acaccaccc agancancca cccgccatgg ggaatgtnt caaggaatcg cngggcaacg 420
tggaactcng tcccnnaagg gggcagaatc tccaatagan gganngaacc cttgctnana 480
aaaaaaaaana aaaaa 495

```

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<210> 95
<211> 472
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(472)
<223> n = A,T,C or G

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<400> 95
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tagctgtttt gagttgatcc gcaccactgc accacaactc aatatgaaaa ctatttnact 180
tattttattat cttgtgaaaa gtatacaatg aaaattttgt tcatactgta ttatcaagt 240
atgatgaaaa gcaatagata tatattcttt tattatgttn aattatgatt gccattatta 300
atcggaacaaa tgtggagtgt atgttctttt cacagtaata tatgcctttt gtaacttcac 360
ttggttattt tattgtaaat gaattacaaa attcttaatt taagaaaatg gtangttata 420
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```

```

<210> 96
<211> 476
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(476)
<223> n = A,T,C or G

```

```

<400> 96
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```

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ttttaactca tgattttttac acacacaatc cagaacttat tatatagcct ctaagtcttt      180
attcttcaca gtagatgatg aaagagtcct ccagtgtctt gngcanaatg ttctagntat      240
agctggatac atacngtggg agttctataa actcatacct cagtgggact naacccaaaat      300
tgtgttagtc tcaattccta ccacactgag ggagcctccc aaatcactat attcttatct      360
gcaggtaact ctccagaaaa acngacaggg caggcttgca tgaaaaagtn acatctgcgt      420
tacaaagtct atcttctctca nangtctgtg aaggaacaat ttaatcttct agcttt      476

```

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<210> 97
<211> 479
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (479)
<223> n = A,T,C or G

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```

<400> 97
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caatcgcaaa tcaaaactca caagtgtctca tctgtttagt atttagtgta ataagactta      180
gattgtgctc cttecgatat gattgtttct canatcttgg gcaatnttcc ttagtcaaat      240
caggctacta gaattctggt attggatatn tgagagcatg aaatttttaa naatacactt      300
gtgattatna aattaatcac aaatttcact tatacctgct atcagcagct agaaaaacat      360
ntnnttttta natcaaagta ttttgtgttt ggaantgtnn aaatgaaatc tgaatgtggg      420
ttcnatctta ttttttccn gacnactant tnttttttta gggncatttc tganccatc      479

```

```

<210> 98
<211> 461
<212> DNA
<213> Homo sapien

```

```

<400> 98
agtgacttgt cctccaacaa aacccttga tcaagtttgt ggactgaca atcagaccta      60
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tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga      180
agtgattcag ttctctctac ggatgagaga ctggctcaag aatatcctca tgcagcttta      240
tgaagccact ctgaacacgc tggttatcta gatgagaaca gagaaataaa gtcagaaaat      300
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ttaagaaaaa ctaccacatg ttgtgtatcc tgggtccggc cgtttatgaa ctgaccaccc      420
tttggaaataa tcttgacgct cctgaacttg ctctctgcg a      461

```

```

<210> 99
<211> 171
<212> DNA
<213> Homo sapien

```

```

<400> 99
gtggcgcgc gcaggtgttt cctcgtaacc cagggccccc tcccttcccc aggcgtccct      60
cggcgccctc gcgggcccga ggaggagcgg ctggcggtg gggggagtgt gaccaccct      120
cggtgagaaa agccttctct agcgatctga gaggcgtgcc ttgggggtac c      171

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<210> 100
<211> 269
<212> DNA
<213> Homo sapien

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<400> 100

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aaggctgagc	tgacgccgca	gaggtcgtgt	cacgtccac	gaccttgacg	ccgtcgggga	180
cagccggaac	agagcccggt	gaagcgggag	gcctcgggga	gcccctcggg	aagggcggcc	240
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<210> 101

<211> 405

<212> DNA

<213> Homo sapien

<400> 101

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ttgattgggt	tgtctttatg	ggggcggggt	ggggtagggg	aaacgaagca	aataacatgg	180
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ctgttctgga	gggagattag	ggtttcttgc	caaatccaac	aaaatccact	gaaaaagtgtg	360
gatgatcagt	acgaataccg	aggcatattc	tcatatcggt	ggcca		405

<210> 102

<211> 470

<212> DNA

<213> Homo sapien

<400> 102

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atatacttct	ttcagcaaac	ttgttacata	aattaaata	atatatacgg	ctgggtgttt
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<210> 103

<211> 581

<212> DNA

<213> Homo sapien

<400> 103

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taaatggaaa	ctgccttaga	tacataattc	ttaggaatta	gcttaaaatc	tgccataaagt	180
gaaaatcttc	tctagctctt	ttgactgtaa	atttttgact	cttgtaaaac	atccaaattc	240
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gcttctctag	cctcatttcc	tagctcttat	ctactattag	taagtggctt	tttctctaaa	360
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<210> 104

<211> 578

<212> DNA

<213> Homo sapien

<400> 104

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aaatcacatt	tacgacagca	ataataaaac	tgaagtacca	gttaaatatc	caaaataatt	480
aaaggaacat	ttttagcctg	ggtataatta	gctaattcac	tttacaagca	tttattagaa	540
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<210> 105

<211> 538

<212> DNA

<213> Homo sapien

<400> 105

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<210> 106

<211> 473

<212> DNA

<213> Homo sapien

<400> 106

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<210> 107

<211> 1621

<212> DNA

<213> Homo sapien

<400> 107

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tggtgagaat	ccgtatgcc	cgctgaatct	cctggctgac	tttgctgggtg	gtggccttat	480
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<210> 108

<211> 382

<212> PRT

<213> Homo sapien

<400> 108

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Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
35     40     45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
50     55     60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65     70     75     80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
85     90     95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
100    105    110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115    120    125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
130    135    140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Leu Met Cys
145    150    155    160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
165    170    175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
180    185    190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
195    200    205
Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
210    215    220
Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
225    230    235    240
Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
245    250    255

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Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
 260 265 270
 Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
 275 280 285
 Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val
 290 295 300
 His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu
 305 310 315 320
 Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala
 325 330 335
 Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu
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<210> 109
 <211> 1524
 <212> DNA
 <213> Homo sapien

<400> 109
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<210> 110
 <211> 3410
 <212> DNA
 <213> Homo sapien

<400> 110
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cccaactttc	ccctaccccc	aactttcccc	accagctcca	caaccctgtt	tggagctact	3060
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tagcgggggtg	aatattttat	actgtaagt	agcaatcaga	gtataatgtt	tatggtgaca	3300
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aaaaaaaaara	aaaaaaaaaa	aaaaaaaaaa	aaaaaaataa	aaaaaaaaaa		3410

<210> 111

<211> 1289

<212> DNA

<213> Homo sapien

<400> 111

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agccaggcgt ccctctgcct gccactcag tggcaacacc cgggagctgt tttgtccttt      60
gtggagcctc agcagttccc tctttcagaa ctactgccca agagccctga acaggagcca      120
ccatgcagtg cttcagcttc attaaacca tgatgatcct cttcaatttg ctcatctttc      180
tgtgtggtgc agccctggtg gcagtgggca tctgggtgtc aatcgatggg gcacaccttc      240
tgaagatctt cgggccactg tcgtccagtg ccatgcagtt tgtcaacgtg ggctacttcc      300
tcatcgcagc cggcgttgtg gtctttgtct ttggtttcct gggctgctat ggtgctaaga      360
ctgagagcaa gtgtgccctc gtgacgttct tcttcacctc cctcctcatc ttcattgctg      420
aggttgacgc tgctgtggtc gccttggtgt acaccacaat ggctgagcac ttcctgacgt      480
tgctggtagt gcctgccatc aagaaagatt atggttccca ggaagacttc actcaagtgt      540
ggaacaccac catgaaaggg ctcaagtgtc gtggcttcac caactatacg gatattgagg      600
actacccta cttcaaagag aacagtgcct ttccccatt ctgttgcaat gacaacgtca      660
ccaacacagc caatgaaacc tgcaccaagc aaaaggctca cgacaaaaaa gtagaggggt      720
gcttcaatca gcttttgtat gacatccgaa ctaatgcagt caccgtgggt ggtgtggcag      780
ctggaattgg gggcctcgag ctggctgcca tgattgtgtc catgtatctg tactgcaatc      840
tacaataagt ccacttctgc ctctgccact actgctgcca catgggaact gtgaagaggc      900
accctggcaa gcagcagtga ttgggggagg ggacaggatc taacaatgtc acttgggcca      960
gaatggacct gccctttctg ctccagactt ggggctagat agggaccact ccttttagcg      1020
atgcctgact ttcttccat tgggtgggtg atgggtgggg ggcattccag agcctctaag      1080
gtagccagtt ctgttgccca ttccccagt ctattaaacc cttgatatgc cccctaggcc      1140
tagtggtgat cccagtgtc tactggggga tgagagaaag gcattttata gcctgggcat      1200
aagtgaatc agcagagcct ctgggtggat gtgtagaagg cacttcaaaa tgcataaacc      1260
tgttacaatg ttaaaaaaaaa aaaaaaaaaa      1289

```

<210> 112

<211> 315

<212> PRT

<213> Homo sapien

<400> 112

```

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
 1           5           10           15
Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
 20           25           30
Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
 35           40           45
Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
 50           55           60
Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
 65           70           75           80
Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
 85           90           95
Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
100           105           110
Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Leu Val Ile Phe
115           120           125
Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
130           135           140
Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
145           150           155           160
Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
165           170           175
Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
180           185           190
Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu

```

195	200	205
His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr		
210	215	220
Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp		
225	230	235
Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val		
245	250	255
Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg		
260	265	270
Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly		
275	280	285
Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly		
290	295	300
Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp		
305	310	315

<210> 113

<211> 553

<212> PRT

<213> Homo sapien

<400> 113

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala		
1	5	10
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu		
20	25	30
Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val		
35	40	45
Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly		
50	55	60
Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly		
65	70	75
Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile		
85	90	95
Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu		
100	105	110
Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly		
115	120	125
Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu		
130	135	140
Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala		
145	150	155
Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr		
165	170	175
Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu		
180	185	190
Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu		
195	200	205
Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly		
210	215	220
Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His		
225	230	235
Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu		
245	250	255
Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg		
260	265	270
Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe		
275	280	285

Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
 290 295 300
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
 305 310 315 320
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
 325 330 335
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
 340 345 350
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
 355 360 365
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
 370 375 380
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
 385 390 395 400
 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
 405 410 415
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
 420 425 430
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
 435 440 445
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser
 450 455 460
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
 465 470 475 480
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 485 490 495
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
 500 505 510
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
 515 520 525
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp
 530 535 540
 Lys Ser Asp Leu Ala Lys Tyr Ser Ala
 545 550

<210> 114
 <211> 241
 <212> PRT
 <213> Homo sapien

<400> 114
 Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
 1 5 10 15
 Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
 20 25 30
 Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
 35 40 45
 Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
 50 55 60
 Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
 65 70 75 80
 Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile
 85 90 95
 Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr
 100 105 110
 Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys
 115 120 125
 Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met

130	135	140
Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp		
145	150	155
Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn		160
	165	170
Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala		175
	180	185
His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile		190
	195	200
Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly		205
	210	220
Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu		
225	230	235
Gln		240

<210> 115
 <211> 366
 <212> DNA
 <213> Homo sapien

<400> 115
 gctctttctc tcccctcctc tgaatttaaat tcttttcaact tgcaatttgc aaggattaca 60
 catttcactg tgatgtatat tgtgttgcaa aaaaaaaaaa gtgtctttgt ttaaaattac 120
 ttggtttggt aatccatctt gctttttccc cattggaaact agtcattaac ccatctctga 180
 actggtagaa aaacatctga agagctagtc tatcagcatc tgacagggtga attggatggg 240
 tctcagaacc atttcaccca gacagcctgt ttctatcctg tttaataaat tagtttgggt 300
 tctctacatg cataacaaac cctgctccaa tctgtcacat aaaagtctgt gacttgaagt 366
 ttagtc

<210> 116
 <211> 282
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(282)
 <223> n = A,T,C or G

<400> 116
 acaaagatga accatttctc atattatagc aaaattaaaa tctaccgta ttctaattatt 60
 gagaaatgag atnaaacaca atnttataaa gtctacttag agaagatcaa gtgacctcaa 120
 agactttact attttcatat tttaagacac atgatttatc ctattttagt aacctgggtc 180
 atacgttaaa caaaggataa tgtgaacagc agagaggatt tgttggcaga aaatctatgt 240
 tcaatctnga actatctana tcacagacat ttctattcct tt 282

<210> 117
 <211> 305
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(305)
 <223> n = A,T,C or G

<400> 117

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acacatgtcg cttcactgcc ttcttagatg cttctgggtca acatanagga acagggacca      60
tatttatcct ccctcctgaa acaattgcaa aataanacaa aatatatgaa acaattgcaa      120
aataaggcaa aatatatgaa acaacaggtc tcgagatatt ggaaatcagt caatgaagga      180
tactgatccc tgatcactgt cctaattgcag gatgtgggaa acagatgagg tcacctctgt      240
gactgccccca gcttactgcc tgtagagagt ttctangctg cagttcagac agggagaaat      300
tggtg      305

```

<210> 118

<211> 71

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(71)

<223> n = A,T,C or G

<400> 118

```

accaaggtgt ntgaatctct gacgtgggga tctctgattc ccgcacaatc tgagtggaaa      60
aantcctggg t      71

```

<210> 119

<211> 212

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(212)

<223> n = A,T,C or G

<400> 119

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actccggttg gtgtcagcag cacgtggcât tgaacatngc aatgtggagc ccaaaccaca      60
gaaaatgggg tgaaattggc caactttcta tnaacttatg ttggcaantt tgccaccaac      120
agtaagctgg ccttctaat aaaagaaaat tgaaagggtt ctcactaanc ggaattaant      180
aatggantca aganactccc aggctcagc gt      212

```

<210> 120

<211> 90

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(90)

<223> n = A,T,C or G

<400> 120

```

actcgttgca natcaggggc cccccagagt caccgttgca ggagtccttc tggctcttgcc      60
ctccgccggc gcagaacatg ctgggggtggt      90

```

<210> 121

<211> 218

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (218)

<223> n = A,T,C or G

<400> 121

tgtancgtga	anacgacaga	nagggttgtc	aaaaatggag	aanccttgaa	gtcattttga	60
gaataagatt	tgctaaaaga	tttggggcta	aaacatgggt	attgggagac	atttctgaag	120
atatncangt	aaattangga	atgaattcat	ggttcttttg	ggaattcctt	tacgatngcc	180
agcatanact	tcatgtgggg	atancagcta	cccttgta			218

<210> 122

<211> 171

<212> DNA

<213> Homo sapien

<400> 122

taggggtgta	tgcaactgta	aggacaaaaa	ttgagactca	actggcttaa	ccaataaagg	60
catttggttag	ctcatggaac	aggaagtcgg	atggtggggc	atcttcagtg	ctgcatgagt	120
caccaccccg	gcgggggtcat	ctgtgccaca	ggtccctggt	gacagtgcgg	t	171

<210> 123

<211> 76

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (76)

<223> n = A,T,C or G

<400> 123

tgtagcgtga	agacnacaga	atggtgtgtg	ctgtgctatc	caggaacaca	tttattatca	60
ttatcaanta	ttgtgt					76

<210> 124

<211> 131

<212> DNA

<213> Homo sapien

<400> 124

acctttcccc	aaggccaatg	tctgtgtgtc	taactggccg	gctgcaggac	agctgcaatt	60
caatgtgctg	ggtcatatgg	aggggaggag	actctaaaat	agccaatttt	attctcttgg	120
ttaagatttg	t					131

<210> 125

<211> 432

<212> DNA

<213> Homo sapien

<400> 125

actttatcta	ctggctatga	aatagatggt	ggaaaattgc	gttaccaact	ataccactgg	60
cttgaaaaag	aggtgatagc	tcttcagagg	acttgtgact	tttgctcaga	tgctgaagaa	120
ctacagtctg	catttggcag	aatgaagat	gaatttggat	taaatgagga	tgctgaagat	180
ttgcctcacc	aaacaaaagt	gaaacaactg	agagaaaatt	ttcaggaaaa	aagacagtgg	240
ctcttgaaat	atcagtcact	tttgagaatg	tttcttagtt	actgcatact	tcatggatcc	300
catggtgggg	gtcttgcata	tgtaagaatg	gaattgattt	tgcttttgca	agaatctcag	360
caggaaacat	cagaaccact	atcttctagc	cctctgtcag	agcaaacctc	agtgccctctc	420
ctctttgctt	gt					432

<210> 126
 <211> 112
 <212> DNA
 <213> Homo sapien

<400> 126
 acacaacttg aatagtaaaa tagaaactga gctgaaattt ctaattcact ttctaaccat 60
 agtaagaatg atatttcccc ccagggatca ccaaataattt ataaaaattt gt 112

<210> 127
 <211> 54
 <212> DNA
 <213> Homo sapien

<400> 127
 accacgaaac cacaacaag atggaagcat caatccactt gccaaagcaca gcag 54

<210> 128
 <211> 323
 <212> DNA
 <213> Homo sapien

<400> 128
 acctcattag taattgtttt gttgtttcat ttttttctaa tgtctcccct ctaccagctc 60
 acctgagata acagaatgaa aatggaagga cagccagatt tctcctttgc tctctgctca 120
 ttctctctga agtctagggt acccattttg gggacccatt ataggcaata aacacagtgc 180
 ccaaagcatt tggacagttt cttgttgtgt tttagaatgg ttttcctttt tcttagcctt 240
 ttcttgcaaa aggtcactc agtccttgc ttgctcagtg gactgggctc cccagggcct 300
 aggtgcctt cttttccatg tcc 323

<210> 129
 <211> 192
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(192)
 <223> n = A,T,C or G

<400> 129
 acatacatgt gtgtatatat ttaaatatca cttttgtatc actctgactt tttagcatac 60
 tgaaaacaca ctaacataat ttntgtgaac catgatcaga tacaaccaa atcattcatc 120
 tagcacattc atctgtgata naaagatagg tgagtttcat ttccttcacg ttggccaatg 180
 gataaacaaa gt 192

<210> 130
 <211> 362
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(362)
 <223> n = A,T,C or G

<400> 130
 ccctttttta tggaatgagt agactgtatg tttgaanatt tanccacaac ctctttgaca 60


```

tataatgacg caacaaaaag gtgctgttta gtcctatggt tcagtttatg cccttgacaa    120
gtttccattg tgttttgccg atcttctggc taatcgtggt atcctccatg ttattagtaa    180
ttctgtattc cattttgtta acgcctggta gatgtaacct gctangaggc taactttata    240
cttatttaaa agctcttatt ttgtgggtcat taaaatggca atttatgtgc agcactttat    300
tgcagcagga agcacgtgtg ggttggttgt aaagctcttt gctaattcta aaaagtaatg    360
gg

```

<210> 131

<211> 332

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (332)

<223> n = A,T,C or G

<400> 131

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ctttttgaaa gatcgtgtcc actcctgtgg acatcttgtt ttaatggagt ttcccatgca    60
gtangactgg tatggttgca gctgtccaga taaaaacatt tgaagagctc caaaatgaga    120
gttctcccag gttcgccctg ctgctccaag tctcagcagc agcctctttt aggaggcatc    180
ttctgaacta gattaaggca gcttgtaaat ctgatgtgat ttggtttatt atccaactaa    240
cttccatctg ttatcactgg agaaagccca gactcccan gacnggtacg gattgtgggc    300
atanaaggat tgggtgaagc tggcgttgtg gt

```

<210> 132

<211> 322

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (322)

<223> n = A,T,C or G

<400> 132

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acttttgcca ttttgtatat ataaacaatc ttgggacatt ctctgaaaa ctaggtgtcc    60
agtggctaag agaactcgat ttcaagcaat tctgaaagga aaaccagcat gacacagaat    120
ctcaaattcc caaacagggg ctctgtggga aaaatgaggg aggacctttg tatctcgggt    180
tttagcaagt taaaatgaan atgacaggaa aggcttattt atcaacaaag agaagagttg    240
ggatgcttct aaaaaaaact ttggtagaga aaataggaat gctnaatcct agggaagcct    300
gtaacaatct acaattggtc ca

```

<210> 133

<211> 278

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (278)

<223> n = A,T,C or G

<400> 133

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acaagccttc acaagtttaa ctaaattggg attaatcttt ctgtanttat ctgcataatt    60
cttgtttttc tttccatctg gctcctgggt tgacaatttg tggaacaac tctattgcta    120
ctattttaaaa aaatcacaa atctttccct ttaagctatg ttnaattcaa actattcctg    180
ctattcctgt tttgtcaaag aaattatatt tttcaaaata tgtntatttg tttgatgggt    240

```

cccacgaaac actaataaaa accacagaga ccagcctg 278

<210> 134
 <211> 121
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(121)
 <223> n = A,T,C or G

<400> 134
 gtttanaaaa cttgttttagc tccatagagg aaagaatggt aaactttgta ttttaaaaca 60
 tgattctctg aggttaaact tggttttcaa atgttatatt tacttgatt ttgcttttgg 120
 t 121

<210> 135
 <211> 350
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(350)
 <223> n = A,T,C or G

<400> 135
 acttanaacc atgcctagca catcagaatc cctcaaagaa catcagtata atcctataacc 60
 atancaagtg gtgactggtt aagcgtgcga caaaggtcag ctggcacatt acttgtgtgc 120
 aaacttgata cttttgttct aagtaggaac tagtatacag tncctaggan tggtagtcca 180
 ggggtgcccc caactcctgc agccgtcct ctgtgccagn cctgnaagg aactttcgct 240
 ccacatcaat caagccctgg gccatgctac ctgcaattgg ctgaacaaac gtttgctgag 300
 ttcccaagga tgcaaaacct ggtgctcaac tcctggggcg tcaactcagt 350

<210> 136
 <211> 399
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(399)
 <223> n = A,T,C or G

<400> 136
 tgtaccgtga agacgacaga agttgcatgg cagggacagg gcagggccga ggccagggtt 60
 gctgtgattg tatccgaata ntctcgtga gaaaagataa tgagatgacg tgagcagcct 120
 gcagacttgt gtctgccttc aanaagccag acaggaaggc cctgcctgcc ttggctctga 180
 cctggcgccc agccagccag ccacagggtg gcttcttctt ttgtggtga caacnccaag 240
 aaaactgcag aggccaggg tcagggtgna gtgggtangt gaccataaaa caccagggtg 300
 tcccaggaac ccgggcaaag gccatcccca cctacagcca gcatgcccac tggcgtgatg 360
 ggtgcagang gatgaagcag ccagntgttc tgctgtggt 399

<210> 137
 <211> 165
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(165)
 <223> n = A,T,C or G

<400> 137
 actggtgtgg tngggggtga tgctggtggt anaagttgan gtgacttcan gatggtgtgt 60
 ggaggaagtg tgtgaacgta gggatgtaga ngttttggcc gtgctaaatg agcttcggga 120
 ttggctgggc ccaactggtg tcaactgtcat tgggtggggt cctgt 165

<210> 138
 <211> 338
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(338)
 <223> n = A,T,C or G

<400> 138
 actcactgga atgccacatt cacaacagaa tcagaggtct gtgaaaacat taatggctcc 60
 ttaacttctc cagtaagaat cagggacttg aaatggaaac gttaacagcc acatgcccaa 120
 tgctgggagc tctcccatgc ctccacagt gaaagggctt gagaaaaatc acatccaatg 180
 tcatgtgttt ccagccacac caaaaggtgc ttggggtgga gggctggggg catananggt 240
 cangcctcag gaagcctcaa gtccattca gctttgccac tgtacattcc ccatntttaa 300
 aaaaactgat gccttttttt tttttttttg taaaattc 338

<210> 139
 <211> 382
 <212> DNA
 <213> Homo sapien

<400> 139
 gggaatcttg gtttttggca tctggtttgc ctatagccga ggccactttg acagaacaaa 60
 gaaagggact tcgagtaaga aggtgattta cagccagcct agtgcccgaa gtgaaggaga 120
 attcaaacag acctcgtcat tcctggtgtg agcctggtcg gctcaccgcc tatcatctgc 180
 atttgctta ctcagggtgt accggactct ggccctgat gtctgtagt ttacaggatg 240
 ccttatttgc ctctacacc ccacagggcc cctacttct tcggatgtgt ttttaataat 300
 gtcagctatg tgcccatcc tccttcattgc cctccctccc tttctacca ctgctgagt 360
 gcctggaact tgtttaaagt gt 382

<210> 140
 <211> 200
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(200)
 <223> n = A,T,C or G

<400> 140
 accaaanctt ctttctgttg tgttngattt tactataggg gtttngcttn ttctaaanat 60
 acttttcatt taacancttt tgttaagtgt caggctgcac tttgtccat anaattattg 120
 ttttcacatt tcaacttgta tgtgtttgtc tcttanagca ttggtgaaat cacatatttt 180
 atattcagca taaaggagaa 200

<210> 141
 <211> 335
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(335)
 <223> n = A,T,C or G

<400> 141
 accttatttt caaaacactc atatgttgca aaaaacacat agaaaaataa agtttggtgg 60
 ggggtgctgac taaacttcaa gtcacagact tttatgtgac agattggagc aggggtttgtt 120
 atgcatgtag agaaccctaaa ctaatttatt aaacaggata gaaacaggct gtctgggtga 180
 aatggttctg agaaccatcc aattcacctg tcagatgctg atanactagc tcttcagatg 240
 tttttctacc agttcagaga tnggttaatg actanttcca atgggggaaa agcaagatgg 300
 attcacaac caagtaattt taaacaaaga cactt 335

<210> 142
 <211> 459
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(459)
 <223> n = A,T,C or G

<400> 142
 accagggttaa tattgccaca tatatccttt ccaattgcgg gctaaacaga cgtgtattta 60
 ggggtgttta aagacaaccc agcttaatat caagagaaat tgtgaccttt catggagtat 120
 ctgatggaga aaacactgag ttttgacaaa tcttatttta ttcagatagc agtctgatca 180
 cacatgggtcc aacaacactc aaataataaa tcaaataatna tcagatgtta aagattggtc 240
 ttcaaacatc atagccaatg atgccccgct tgcttataat ctctccgaca taaaaccaca 300
 tcaaacactc agtggccacc aaaccattca gcacagcttc cttaactgtg agctgtttga 360
 agctaccagt ctgagcacta ttgactatnt ttttcangct ctgaatagct ctagggatct 420
 cagcanggggt gggaggaacc agctcaacct tggcgctant 459

<210> 143
 <211> 140
 <212> DNA
 <213> Homo sapien

<400> 143
 acatttcctt ccaccaagtc aggactcctg gcttctgtgg gagttcttat cacctgaggg 60
 aaatccaaac agtctctcct agaaaggaat agtgtcacca accccaccca tctccctgag 120
 accatccgac ttccctgtgt 140

<210> 144
 <211> 164
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(164)
 <223> n = A,T,C or G

<400> 144
 acttcagtaa caacatacaa taacaacatt aagtgtatat tgccatcttt gtcattttct 60
 atctatacca ctctcccttc tgaaaacaan aatcactanc caatcactta tacaaatttg 120
 aggcaattaa tccatatttg ttttcaataa ggaaaaaaag atgt 164

<210> 145
 <211> 303
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(303)
 <223> n = A,T,C or G

<400> 145
 acgtagacca tccaactttg tatttgtaat ggcaaacatc cagnagcaat tcctaaacaa 60
 actggagggt atttataccc aattatccca ttcattaaca tgccctcctc ctcaggctat 120
 gcaggacagc tatcataagt cggcccaggc atccagatac taccatttgt ataaacttca 180
 gtaggggagt ccatccaagt gacaggctta atcaaaggag gaaatggaac ataaagccag 240
 tagtaaaatn ttgcttagct gaaacagcca caaaagactt accgcctggg tgattaccat 300
 caa 303

<210> 146
 <211> 327
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(327)
 <223> n = A,T,C or G

<400> 146
 actgcagctc aattagaagt ggtctctgac tttcatcanc ttctccctgg gctccatgac 60
 actggcctgg agtgactcat tgctctgggt gggtgagaga gctcctttgc caacaggcct 120
 ccaagtcagg gctgggattt gtttcccttc cacattctag caacaatatg ctggccactt 180
 cctgaacagg gagggtgga ggagccagca tggaacaagc tgccactttc taaagtagcc 240
 agacttgccc ctgggcctgt cacacctact gatgaccttc tgtgcctgca ggatggaatg 300
 taggggtgag ctgtgtgact ctatggt 327

<210> 147
 <211> 173
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(173)
 <223> n = A,T,C or G

<400> 147
 acattgtttt tttgagataa agcattgana gagctctcct taacgtgaca caatggaagg 60
 actggaacac ataccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt 120
 atattcaagc acatatgtta tatattattc agttccatgt ttatagccta gtt 173

<210> 148

<211> 477
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(477)
 <223> n = A,T,C or G

<400> 148
 acaaccactt tatctcatcg aatttttaac ccaaactcac tcactgtgcc tttctatcct 60
 atgggatata ttatttgatg ctccatttca tcacacatat atgaataata cactcatact 120
 gccctactac ctgctgcaat aatcacattc ctttcctgtc ctgaccctga agccattggg 180
 gtggtcctag tggccatcag tccangcctg caccttgagc ccttgagctc cattgctcac 240
 nccanccac ctcaccgacc ccatcctctt acacagctac ctccttgctc tctaacccca 300
 tagattatnt ccaaattcag tcaattaagt tactattaac actctacccg acatgtccag 360
 caccactggg aagccttctc cagccaacac acacacacac acacncacac acacacatat 420
 ccaggcacag gctacctcat cttcacaatc acccctttaa ttaccatgct atggtgg 477

<210> 149
 <211> 207
 <212> DNA
 <213> Homo sapien

<400> 149
 acagttgtat tataatatca agaaataaac ttgcaatgag agcatttaag agggaagaac 60
 taacgtatatt tagagagcca aggaagggtt ctgtggggag tgggatgtaa ggtggggcct 120
 gatgataaat aagagtcagc caggttaagt ggtggtgtgg tatgggcaca gtgaagaaca 180
 tttcaggcag agggaacagc agtgaata 207

<210> 150
 <211> 111
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(111)
 <223> n = A,T,C or G

<400> 150
 accttgattt cattgctgct ctgatggaaa cccaactatc taatttagct aaaacatggg 60
 cacttaaatg tggtcagtgt ttggacttgt taactantgg catctttggg t 111

<210> 151
 <211> 196
 <212> DNA
 <213> Homo sapien

<400> 151
 agcgcggcag gtcatatga acattccaga tacctatcat tactcgatgc tggtgataac 60
 agcaagatgg ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaaccat 120
 ggataccaac cggaataccc ctatcccgcg cagcccactg tgggtcccccac tgtctacgag 180
 gtgcatccgg ctacgt 196

<210> 152
 <211> 132
 <212> DNA

<213> Homo sapien

<400> 152

acagcacttt cacatgtaag aagggagaaa ttcctaaatg taggagaaag ataacagAAC	60
cttccccttt tcattctagt gtggaaacct gatgctttat gttgacagga atagaaccag	120
gagggagttt gt	132

<210> 153

<211> 285

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(285)

<223> n = A,T,C or G

<400> 153

acaanaccca nganaggcca ctggccgtgg tgtcatggcc tccaaacatg aaagtgtcag	60
cttctgtctt tatgtcctca tctgacaact ctttaccatt tttatcctcg ctcagcagga	120
gcacatcaat aaagtccaaa gtcttggact tggccttggc ttggaggaag tcatcaacac	180
cctggctagt gaggggtgcg cgccgctcct ggatgacggc atctgtgaag tcgtgcacca	240
gtctgcaggc cctgtggaag cgccgtccac acggagtnag gaatt	285

<210> 154

<211> 333

<212> DNA

<213> Homo sapien

<400> 154

accacagtcc tggtgggcca gggettcattg accctttctg tgaaaagcca tattatcacc	60
accccaaat tttccttaaa tatctttaac tgaaggggtc agcctcttga ctgcaaagac	120
cttaagccgg ttacacagct aactcccact ggccttgatt tgtgaaattg ctgctgcctg	180
attggcacag gagtgcgaagg tgttcagctc ccctcctccg tggaacgaga ctctgatttg	240
agtttcacaa attctcgggc cacctcgtca ttgctcctct gaaataaaat ccggagaatg	300
gtcaggcctg tctcatccat atggatcttc cgg	333

<210> 155

<211> 308

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(308)

<223> n = A,T,C or G

<400> 155

actggaata ataaaaccca catcacagtg ttgtgtcaaa gatcatcagg gcatggatgg	60
gaaagtgtt tgggaactgt aaagtgccta acacatgatc gatgattttt gttataatat	120
ttgaatcacg gtgcatacaa actctcctgc ctgctcctcc tgggccccag cccagcccc	180
atcacagctc actgctctgt tcatccaggc ccagcatgta gtggctgatt cttcttggct	240
gcttttagcc tccanaagtt tctctgaagc caaccaaac tctangtgta aggcattgctg	300
gccttgg	308

<210> 156

<211> 295

<212> DNA

<213> Homo sapien

<400> 156

accttgctcg	gtgcttgga	catattagga	actcaaaata	tgagatgata	acagtgccta	60
ttattgatta	ctgagagaac	tgtagacat	ttagttgaag	atcttctaca	caggaactga	120
gaataggaga	ttatgtttgg	ccctcatatt	ctctcctatc	ctccttgccct	cattctatgt	180
ctaataatatt	ctcaatcaaa	taaggttagc	ataatcagga	aatcgaccaa	ataccaatat	240
aaaaccagat	gtctatcctt	aagattttca	aatagaaaac	aaattaacag	actat	295

<210> 157

<211> 126

<212> DNA

<213> Homo sapien

<400> 157

acaagttaa	atagtgtgt	cactgtgcat	gtgctgaaat	gtgaaatcca	ccacatttct	60
gaagagcaa	acaaattctg	tcattgtaac	tctatcttgg	gtcgtgggta	tatctgtccc	120
cttagt						126

<210> 158

<211> 442

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(442)

<223> n = A,T,C or G

<400> 158

accactggg	cttgaaaaca	cccatcctta	atacgatgat	ttttctgtcg	tgtgaaaatg	60
aanccagcag	gctgccccta	gtcagtcctt	ccttccagag	aaaaagagat	ttgagaaaagt	120
gcctgggtaa	ttcaccatta	atttctcccc	ccaaactctc	tgagtcttcc	cttaatatatt	180
ctggtggttc	tgaccaaagc	aggtcatggt	ttgttgagca	tttgggatcc	cagtgaagta	240
natgtttgta	gccttgcata	cttagccctt	cccacgcaca	aacggagtgg	cagagtgggtg	300
ccaaccctgt	tttcccagtc	cacgtagaca	gattcacagt	gcggaattct	ggaagctgga	360
nacagacggg	ctctttgcag	agccgggact	ctgagangga	catgagggcc	tctgcctctg	420
tgttcattct	ctgatgtcct	gt				442

<210> 159

<211> 498

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(498)

<223> n = A,T,C or G

<400> 159

acttccagg	aacgttggtg	tttccgttga	gcctgaactg	atgggtgacg	ttgtaggttc	60
tccaacaaga	actgaggttg	cagagcgggt	agggaaagag	gctgttccag	ttgcacctgg	120
gctgctgtgg	actgttggtg	attctcact	acggccaag	gttggtggaac	tggcanaaag	180
gtgtgtgtt	gganttgagc	tcgggcggct	gtggtagggt	gtgggtctct	caacaggggc	240
tgctgtggg	ccgggangtg	aangtggtgt	gtcacttgag	cttggccagc	tctggaaagt	300
antanattct	tcctgaaggc	cagcgttgt	ggagctggca	ngggtcantg	ttgtgtgtaa	360
cgaaccagtg	ctgctgtggg	tgggtgtana	tcctccacaa	agcctgaagt	tatggtgtcn	420
tcaggtaana	atgtggtttc	agtgtccctg	ggcngctgtg	gaaggttgta	nattgtcacc	480

aaggggaataa gctgtggt

498

<210> 160

<211> 380

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(380)

<223> n = A,T,C or G

<400> 160

acctgcatcc agcttccctg ccaaactcac aaggagacat caacctctag acagggaaac	60
agcttcagga tacttccagg agacagagcc accagcagca aaacaaatat tcccatgcct	120
ggagcatggc atagaggaag ctganaaatg tggggctctga ggaagccatt tgagtctggc	180
cactagacat ctcatcagcc acttgtgtga agagatgccc catgacccca gatgcctctc	240
ccacccttac ctccatctca cacacttgag ctttccactc tgtataattc taacatcctg	300
gagaaaaatg gcagtttgac cgaacctggt cacaacggta gaggctgatt tctaacgaaa	360
cttgtagaat gaagcctgga	380

<210> 161

<211> 114

<212> DNA

<213> Homo sapien

<400> 161

actccacatc ccctctgagc aggcggttgt cgttcaaggt gtatttggcc ttgcctgtca	60
cactgtccac tggccctta tccacttggt gcttaatccc tcgaaagagc atgt	114

<210> 162

<211> 177

<212> DNA

<213> Homo sapien

<400> 162

actttctgaa tcgaatcaaa tgatacttag tgtagtttta atatcctcat atatatcaaa	60
gttttactac tctgataatt ttgtaaacca ggtaaccaga acatccagtc atacagcttt	120
tggtgatata taacttggca ataaccagc ctggtgatac ataaaactac tcaactgt	177

<210> 163

<211> 137

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(137)

<223> n = A,T,C or G

<400> 163

catttataca gacaggcgtg aagacattca cgacaaaaac gcgaaattct atcccgtgac	60
canagaaggc agctacggct actcctacat cctggcgtgg gtggccttcg cctgcacctt	120
catcagcggc atgatgt	137

<210> 164

<211> 469

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(469)

<223> n = A,T,C or G

<400> 164

cttatcacaa tgaatgttct cctgggcagc gttgtgatct ttgccacctt cgtgacttta	60
tgcaatgcat catgctatct catacctaata gagggagttc caggagattc aaccaggaaa	120
tgcatggatc tcaaaggaaa caaacaccca ataaactcgg agtggcagac tgacaactgt	180
gagacatgca cttgctacga aacagaaatt tcatgttgca cccttgtttc tacacctgtg	240
ggttatgaca aagacaactg ccaaagaatc ttcaagaagg aggactgcaa gtatatcgtg	300
gtggagaaga aggaccctaa aaagacctgt tctgtcagt aatggataat ctaatgtgct	360
tctagttagc acagggtcc caggccaggc ctcattctcc tctggcctct aatagtcaat	420
gattgtgtag ccatgcctat cagtaaaaag atntttgagc aaacacttt	469

<210> 165

<211> 195

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(195)

<223> n = A,T,C or G

<400> 165

acagtttttt atanatatcg acattgccgg cacttgtgtt cagtttcata aagctgggtg	60
atccgctgtc atccactatt ccttggctag agtaaaaatt attcttatag cccatgtccc	120
tgaggccgc cgcgccgtag ttctcggtcc agtcgtcttg gcacacaggg tgccaggact	180
tcctctgaga tgagt	195

<210> 166

<211> 383

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(383)

<223> n = A,T,C or G

<400> 166

acatcttagt agtgtggcac atcagggggc catcagggtc acagtcactc atagcctcgc	60
cgaggctgga gtccacacca ccggtgtagg tgtgctcaat cttgggcttg gcgcccacct	120
ttggagaagg gatatgctgc acacacatgt ccacaaagcc tgtgaactcg ccaaagaatt	180
tttgagacc agcctgagca aggggcggat gttcagcttc agtcctcct tcgtcagggtg	240
gatgccaacc tcgtctangg tccgtgggaa gctgggtgtc acntcaccta caacctgggc	300
gangatctta taaagaggct ccnagataaa ctccacgaaa cttctctggg agctgctagt	360
nggggccttt ttggtgaact ttc	383

<210> 167

<211> 247

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature
 <222> (1) ... (247)
 <223> n = A,T,C or G

<400> 167
 acagagccag accttggcca taaatgaanc agagattaag actaaacccc aagtcganat 60
 tggagcagaa actggagcaa gaagtgggcc tggggctgaa gtagagacca aggccactgc 120
 tatanccata cacagagcca actctcaggc caaggcnatg gttggggcag anccagagac 180
 tcaatctgan tccaaagtgg tggctggaac actggtcatg acanaggcag tgactctgac 240
 tgangtc 247

<210> 168
 <211> 273
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (273)
 <223> n = A,T,C or G

<400> 168
 acttctaagt tttctagaag tggaaggatt gtantcatcc tgaaaatggg tttacttcaa 60
 aatccctcan ccttggtctt cactactgtc tatactgana gtgtcatgtt tccacaaagg 120
 gctgacacct gagcctgnat tttcactcat ccctgagaag ccctttccag taggggtgggc 180
 aattcccaac ttccttgcca caagcttccc aggctttctc ccctggaaaa ctccagcttg 240
 agtcccatgat acatcatggt gctgccttgg gca 247

<210> 169
 <211> 431
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (431)
 <223> n = A,T,C or G

<400> 169
 acagccttgg cttccccaaa ctccacagtc tcagtgcaga aagatcatct tccagcagtc 60
 agctcagacc aggggtcaaag gatgtgacat caacagtttc tggtttcaga acagggttcta 120
 ctactgtcaa atgaccccc atacttctc aaaggctgtg gtaagttttg cacagggtgag 180
 ggcagcagaa aggggggtant tactgatgga caccatcttc tctgtatact ccacactgac 240
 cttgccatgg gcaaaggccc ctaccacaaa aacaatagga tcaactgctgg gcaccagctc 300
 acgcacatca ctgacaaccg ggatggaaaa agaantgcc aacttcatac atccaactgg 360
 aaagtgatct gatactggat tcttaattac cttcaaaagc ttctgggggc catcagctgc 420
 tcgaacactg a 431

<210> 170
 <211> 266
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (266)
 <223> n = A,T,C or G

<400> 170
 acctgtgggc tgggctgtta tgcctgtgcc ggctgtgaa agggagttca gaggtggagc 60
 tcaaggagct ctgcaggcat tttgccaanc ctctccanag canagggagc aacctacact 120
 ccccgctaga aagacaccag attggagtc tgggaggggg agttggggtg ggcatttgat 180
 gtatacttgt cacctgaatg aangagccag agaggaanga gacgaanatg anattggcct 240
 tcaaagctag ggtctggca ggtgga 266

<210> 171
 <211> 1248
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(1248)
 <223> n = A,T,C or G

<400> 171
 ggcagccaaa tcataaacgg cgaggactgc agcccgact cgcagccctg gcaggcggca 60
 ctggtcatgg aaaacgaatt gttctgctcg ggcgtcctgg tgcacccgca gtgggtgctg 120
 tcagccgcac actgtttcca gaagtgaagtg cagagctcct acaccatcgg gctgggcttg 180
 cacagtcttg aggccgacca agagccaggg agccagatgg tggaggccag cctctccgta 240
 cggcaccag agtacaacag acccttgctc gctaacgacc tcatgctcat caagttggac 300
 gaatccgtgt ccgagtctga caccatccgg agcatcagca ttgcttcgca gtgccctacc 360
 gcggggaact ctgctcctcg ttctggctgg ggtctgctgg cgaacggcag aatgcctacc 420
 gtgctgcagt gcgtgaacgt gtcggtggg tctgaggagg tctgcagtaa gctctatgac 480
 ccgctgtacc accccagcat gttctgcgcc ggcggagggc aagaccagaa ggactcctgc 540
 aacggtgact ctggggggcc cctgatctgc aacgggtact tgcagggcct tgtgtctttc 600
 ggaaaagccc cgtgtggcca agttggcgtg ccagggtgtct acaccaacct ctgcaaattc 660
 actgagtgga tagagaaaac cgtccaggcc agttaactct ggggactggg aacccatgaa 720
 attgaccccc aaatacatcc tgcggaagga attcaggaat atctgttccc agccccctct 780
 ccctcaggcc caggagtcca ggccccagc ccctcctccc tcaaaccaag ggtacagatc 840
 ccagccct cctccctcag acccaggagt ccagacccc cagccctcc tccctcagac 900
 ccaggagtcc agccccctcc cctcagacc caggagtcca gacccccag cccctcctcc 960
 ctcagacca ggggtccagg cccccaaccc ctctcctcc agactcagag gtccaagccc 1020
 ccaaccntc attccccaga ccagagggtc cagggtccag cccctentcc ctcagacca 1080
 gcggtccaat gccacctaga ctntccctgt acacagtgcc ccttgtggc acgttgacct 1140
 aacctacca gttggttttt catttttngt cccttcccc tagatccaga aataaagttt 1200
 aagagaagng caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1248

<210> 172
 <211> 159
 <212> PRT
 <213> Homo sapien

<220>
 <221> VARIANT
 <222> (1)...(159)
 <223> Xaa = Any Amino Acid

<400> 172
 Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
 1 5 10 15
 Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
 20 25 30
 Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
 35 40 45
 Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly

50	55	60
Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu		
65	70	75
Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe		80
	85	90
Cys Ala Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser		95
	100	105
Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe		110
	115	120
Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn		125
	130	135
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser		140
145	150	155

<210> 173

<211> 1265

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(1265)

<223> n = A,T,C or G

<400> 173

ggcagcccg	actgcagcc	ctggcaggcg	gcactgggtca	tggaaaacga	attgttctgc	60
tcgggcgtcc	tggtgcatcc	gcagtgggtg	ctgtcagccg	cacactgttt	ccagaactcc	120
tacaccatcg	ggctgggect	gcacagtctt	gaggccgacc	aagagccagg	gagccagatg	180
gtggaggcca	gcctctccgt	acggcaccca	gagtacaaca	gaccttgc	cgctaacgac	240
ctcatgctca	tcaagttgga	cgaatccgtg	tccgagtc	acaccatccg	gagcatcagc	300
attgcttcgc	agtgcctac	cgcggggaac	tcttgccctg	ttcttggtg	gggtctgctg	360
gcgaacgggt	agctcacggg	tgtgtgtctg	ccctcttcaa	ggaggtcctc	tgcccagtcg	420
cgggggctga	cccagagctc	tgcgtcccag	gcagaatgcc	taccgtgctg	cagtgcgtga	480
acgtgtcgg	ggtgtctgag	gaggtctgca	gtaagctcta	tgaccgcgtg	taccacccca	540
gcatgttctg	cgccggcgga	gggcaagacc	agaaggactc	ctgcaacgg	gactctgggg	600
ggccccctgat	ctgcaacggg	tacttgacag	gccttgtgtc	tttcggaaaa	gccccgtgtg	660
gccaaagtgg	cgtgccaggt	gtctacacca	acctctgcaa	attcactgag	tggatagaga	720
aaacctgcc	ggccagttaa	ctctggggac	tggaaccca	tgaaattgac	ccccaaatac	780
atcctgcgga	aggaattcag	gaatatctgt	tcccagcccc	tctcctc	ggcccaggag	840
tccaggcccc	cagccccctc	tccctcaaac	caagggtaca	gatccccagc	ccctcctccc	900
tcagaccag	gagtcagac	ccccagccc	ctctcctc	agaccagga	gtccagcccc	960
tctcctc	gacccaggag	tccagacccc	ccagcccc	ctcctcaga	cccaggggtt	1020
gaggccccca	acccctcctc	cttcagagtc	agagggtcaa	gcccccaacc	cctcgttccc	1080
cagaccaga	ggttnaggtc	ccagcccc	ttcctcaga	cccagnggtc	caatgccacc	1140
tagattttcc	ctgnacacag	tgcccccttg	tggnangttg	acccaacctt	accagttggt	1200
ttttcatttt	tngtcccttt	cccctagatc	cagaaataaa	gtttaagaga	ngngcaaaaa	1260
aaaaa						1265

<210> 174

<211> 1459

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(1459)

<223> n = A,T,C or G

<400> 174

```

ggtcagccgc acactgtttc cagaagtgcg tgcagagctc ctacaccatc gggctgggccc 60
tgcacagtct tgaggccgac caagagccag ggagccagat ggtggaggcc agcctctccg 120
tacggcaccac agagtacaac agacccttgc tcgctaacga cctcatgtct atcaagttag 180
acgaatccgt gtccgagtct gacaccatcc ggagcatcag cattgtctcg cagtgcctta 240
ccgcgggggaa ctcttgccct gtttctggct ggggtctgct ggcgaacggt gagctcacgg 300
gtgtgtgtct gccctcttca aggaggtcct ctgcccagtc gggggggctg acccagagct 360
ctgctgcccc ggacagaatgc ctaccgtgct gcagtgcgtg aacgtgtcgg tgggtgtctga 420
ngaggtctgc antaagctct atgacccgct gtaccacccc ancatgttct gcgcggcg 480
agggcaagac cagaaggact cctgcaacgt gagagagggg aaaggggagg gcaggcgact 540
caggggaaggg tggagaaggg ggagacagag acacacaggg ccgcatggcg agatgcagag 600
atggagagac acacagggag acagtgacaa ctagagagag aaactgagag aaacagagaa 660
ataaacacag gaataaagag aagcaaagga agagagaaac agaaacagac atggggaggc 720
agaaacacac acacatagaa atgcagttga ccttccaaca gcatggggcc tgagggcggt 780
gacctccacc caatagaaaa tctctttata acttttgact ccccaaaaac ctgactagaa 840
atagcctact gttgacgggg agccttacca ataacataaa tagtcgattt atgcatacgt 900
tttatgcatt catgatatac ctttgttga attttttgat atttctaagc tacacagttc 960
gtctgtgaat ttttttaaat tgttgcaact ctcctaaaat ttttctgatg tgtttattga 1020
aaaaatccaa gtataagtgg acttgtgcat tcaaaccagg gttgttcaag ggtcaactgt 1080
gtacccagag ggaaacagtg acacagattc atagaggtga aacacgaaga gaaacaggaa 1140
aatcaagac tctacaaaga ggctgggcag ggtggctcat gcctgtaatc ccagcacttt 1200
gggaggcgag gcaggcagat cacttgaggt aaggagtcca agaccagcct ggccaaaatg 1260
gtgaaatcct gtctgtacta aaaatacaaa agtttagctg atatggtggc aggcgcctgt 1320
aatcccagct acttgggagg ctgaggcagg agaattgctt gaatatggga ggcagagggt 1380
gaagtgagtt gagatcacac cactatactc cagctggggc aacagagtaa gactctgtct 1440
caaaaaaaaa aaaaaaaaaa 1459

```

<210> 175

<211> 1167

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(1167)

<223> n = A,T,C or G

<400> 175

```

gcgcagccct ggcaggcggc actggtcatg gaaaacgaat tgttctgtct gggcgtcctg 60
gtgcatccgc agtgggtgct gtcagccgca cactgtttcc agaactccta caccatcggg 120
ctgggcctgc acagtcttga ggccgaccaa gagccaggga gccagatggt ggaggccagc 180
ctctccgtac ggcacccaga gtacaacaga ctcttgtctg ctaacgacct catgctcatc 240
aagttggacg aatccgtgtc cgagtctgac accatccgga gcatcagcat tgcttcgacg 300
tgccctaccg cggggaactc ttgcctcgtt tctggctggg gtctgtctggc gaacggcaga 360
atgcotaccg tgctgcactg cgtgaacgtg tcggtgggtg ctgaggangt ctgcagtaag 420
ctctatgacc cgctgtacca cccagcatg ttctgcgccc gcggagggca agaccagaag 480
gactcctgca acggtgactc tggggggccc ctgatctgca acgggtactt gcagggcctt 540
gtgtcttttc gaaaagcccc gtgtggccaa cttggcgtgc cagggtgtct caccacctc 600
tgcaaatcca ctgagtggat agagaaaacc gtccagncca gtttaactct gggactggga 660
acccatgaaa ttgaccccca aatacatcct gcggaangaa ttcaggaata tctgttccca 720
gcccctcctc cctcaggccc aggagtcacg gcccccagcc cctcctccct caaaccaagg 780
gtacagatcc ccagccctc ctccctcaga cccaggagtc cagacccccc agccctcnt 840
ccntcagacc caggagtcca gcccctcctc cntcagacgc aggagtccag acccccagc 900
ccntentccg tcagaccagc ggggtgcagg ccccaacccc tcntccntca gagtccagag 960
tccaagcccc caacccctcg ttcccagac ccagggtnc aggtcccagc ccctcctccc 1020
tcagaccagc cgttccaatg ccacctagan tntccctgta cacagtgcct ccttgtggca 1080
ngttgacca accttaccag ttggtttttc attttttgc cctttccctt agatccagaa 1140
ataaagtnta agagaagcgc aaaaaaa 1167

```

<210> 176
 <211> 205
 <212> PRT
 <213> Homo sapien

 <220>
 <221> VARIANT
 <222> (1)...(205)
 <223> Xaa = Any Amino Acid

<400> 176
 Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1 5 10 15
 Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
 20 25 30
 Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
 35 40 45
 Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu
 50 55 60
 Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
 65 70 75 80
 Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
 85 90 95
 Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met
 100 105 110
 Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val
 115 120 125
 Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
 130 135 140
 Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
 145 150 155 160
 Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
 165 170 175
 Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
 180 185 190
 Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser
 195 200 205

<210> 177
 <211> 1119
 <212> DNA
 <213> Homo sapien

<400> 177
 gcgcactcgc agccctggca ggcggcactg gtcattggaaa acgaattggt ctgctcgggc 60
 gtcctggtgc atccgcagtg ggtgctgtca gccgcacact gtttccagaa ctctacacc 120
 atcgggctgg gcttcacag tcttgaggcc gaccaagagc caggagacca gatgggtggag 180
 gccagcctct ccgtacggca cccagagtag aacagaccct tgctcgctaa cgacctcatg 240
 ctactcaagt tggacgaatc cgtgtccgag tctgacacca tccggagcat cagcattgct 300
 tcgcagtgcc ctaccgagg gaactcttgc ctcgtttctg gctggggtct gctggcgaac 360
 gatgctgtga ttgccatcca gtcccagact gtgggaggct gggagtgtga gaagctttcc 420
 caaccctggc aggggtgtac catttcggca acttcagtg caaggacgtc ctgctgcac 480
 ctactgggt gctcactact gctcactgca tcaccggaa cactgtgatc aactagccag 540
 caccatagtt ctccgaagtc agactatcat gattactgtg ttgactgtgc tgtctattgt 600
 actaaccatg ccgatgttta ggtgaaatta gcgtcacttg gcctcaacca tcttggtatc 660
 cagttatcct cactgaattg agatttctg cttcagtgtc agccattccc acataatttc 720
 tgacctacag aggtgaggga tcatatagct cttcaaggat gctggtactc ccctcaciaa 780

```

ttcatttctc ctgtttagt gaaaggtgcg cctcttgag cctcccaggg tgggtgtgca      840
ggtcacaatg atgaatgtat gatcgtgttc ccattaccca aagcctttaa atccctcatg      900
ctcagtacac cagggcaggt ctagcatttc ttcatttagt gtatgctgtc cattcatgca      960
accacctcag gactcctgga ttctctgcct agttgagctc ctgcatgctg cctccttggg     1020
gaggtgaggg agagggccca tggttcaatg ggatctgtgc agttgtaaca cattaggtgc     1080
ttaataaaca gaagctgtga tgttaaaaaa aaaaaaaaaa     1119

```

<210> 178

<211> 164

<212> PRT

<213> Homo sapien

<220>

<221> VARIANT

<222> (1)...(164)

<223> Xaa = Any Amino Acid

<400> 178

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1          5          10          15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
 20          25          30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
 35          40          45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
 50          55          60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
 65          70          75          80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
 85          90          95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
100          105          110
Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
115          120          125
Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
130          135          140
Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser
145          150          155          160
Pro Gly Thr Leu

```

<210> 179

<211> 250

<212> DNA

<213> Homo sapien

<400> 179

```

ctggagtgcc ttggtgtttc aagccctgac aggaagcaga atgcaccttc tgaggcacct      60
ccagctgccc ccggccgggg gatgcgaggc tcggagcacc cttgcccggc tgtgattgct     120
gccaggcact gttcatctca gcttttctgt ccctttgtct ccggcaagcg cttctgctga     180
aagttcatat ctggagcctg atgtcttaac gaataaaggt cccatgctcc acccgaaaaa     240
aaaaaaaaaa                                     250

```

<210> 180

<211> 202

<212> DNA

<213> Homo sapien


```

<400> 180
actagtccag tgtggtggaa ttccattgtg ttggggccaa cacaatggct acctttaaca    60
tcaccagac cccgcccctg cccgtgcccc acgctgctgc taacgacagt atgatgctta    120
ctctgctact cggaaactat ttttatgtaa ttaatgtatg ctttcttggt tataaatgcc    180
tgatttaaaa aaaaaaaaaa aa                                           202

```

<210> 181

<211> 558

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(558)

<223> n = A,T,C or G

```

<400> 181
tccytttgkt naggtttkkg agacamccck agacctwaan ctgtgtcaca gacttcyngg    60
aatgtttagg cagtgttagt aatttctytcg taatgattct gttattactt tccnattct    120
ttattcctct ttcttctgaa gattaatgaa gttgaaaatt gaggtggata aatacaaaaa    180
ggtagtgtga tagtataagt atctaagtgc agatgaaagt gtgttatata tatccattca    240
aaattatgca agttagtaat tactcagggt taactaaatt actttaatat gctgttgaaac    300
ctactctggt ccttggttag aaaaaattat aaacaggact ttgttagttt gggaagccaa    360
attgataata ttctatgttc taaaagttgg gctatacata aattattaag aaatatggaw    420
ttttattccc aggaatatgg kgtttcatttt atgaatatta cscrggatag awgtwtgagt    480
aaaaycagtt ttggtwaata ygtwaatatg tcmtaaataa acaakgcttt gacttatttc    540
caaaaaaaaa aaaaaaaaaa                                           558

```

<210> 182

<211> 479

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(479)

<223> n = A,T,C or G

```

<400> 182
acagggwttk grggatgcta agsccccrga rwtygtttga tccaacctg gcttwttttc    60
agaggggaaa atggggccta gaagttacag mscatytagy tgggtgcgmg gcacccctgg    120
cstcacacag astcccaggt agctgggact acaggcacac agtcaactgaa gcaggccctg    180
ttwgcaattc acgttgccac ctccaactta aacattcttc atatgtgatg tccttagtca    240
ctaaggttaa actttccac ccagaaaagg caacttagat aaaatcttag agtactttca    300
tactmttcta agtctcttc cagcctcact kkgagtcctm cytggggggt gataggaant    360
ntctcttggc tttctcaata aartctctat ycatctcatg tttaatgttg tacgcatara    420
awtgstgara aaattaaaat gttctggtty mactttaaaa aaaaaaaaaa aaaaaaaaaa    479

```

<210> 183

<211> 384

<212> DNA

<213> Homo sapien

<400> 183

```

aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactggtgcc    60
agtaccagta ccaataacag tgccagtgcc agtgccagca ccagtgggtg cttcagtgtc    120
ggtgccagcc tgaccgccac tctcacattt gggtctcttc ctggccttgg tggagctggg    180
gccagcacca gtggcagctc tggtgccctg ggtttctcct acaagtgaga ttttagatat    240

```

tgттаатсст gccagtcttt ctcttcaagc cagggtgcat cctcagaaac ctactcaaca	300
cagcactcta ggcagccact atcaatcaat tgaagttgac actctgcatt aratctattt	360
gccatttcaa aaaaaaaaaa aaaa	384

<210> 184

<211> 496

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(496)

<223> n = A,T,C or G

<400> 184

accgaattgg gaccgctggc ttataagcga tcatgttynt ccrgtatkac ctcaacgagc	60
aggagatcg agtctatacg ctgaagaaat ttgacccgat gggacaacag acctgctcag	120
cccattctgc tcggttctcc ccagatgaca aatactctsg acaccgaatc accatcaaga	180
aacgcttcaa ggtgctcatg acccagcaac cgcgccctgt cctctgaggg tcccttaaac	240
tgatgtcttt tctgccacct gttacccttc ggagactccg taaccaaact cttcggactg	300
tgagccctga tgcctttttg ccagccatac tctttggcat ccagtctctc gtggcgattg	360
attatgcttg tgtgaggcaa tcatggtggc atcaccata aagggaacac atttgacttt	420
tttttctcat attttaaatt actacmagaw tattwmagaw waaatgawtt gaaaaactst	480
taaaaaaaaa aaaaaa	496

<210> 185

<211> 384

<212> DNA

<213> Homo sapien

<400> 185

gctggtagcc tatggcgkkg cccacggagg ggctcctgag gccacggrac agtgacttcc	60
caagtatcyt ggcscgctc ttctaccgtc cctacctgca gatcttcggg cagattcccc	120
aggaggacat ggacgtggcc ctcatggagc acagcaactg ytcgtcggag cccggttct	180
gggcacaccc tcttggggcc caggcgggca cctgcgtctc ccagtatgcc aactggcttg	240
tggtgctgct cctcgtcatc ttctgctcgt tggccaacat cctgctggtc aacttgctca	300
ttgccatgtt cagttacaca ttcgcaaaag tacagggcaa cagcgatctc tactgggaag	360
gcgcagcgtt accgectcat ccgg	384

<210> 186

<211> 577

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(577)

<223> n = A,T,C or G

<400> 186

gagttagctc ctccacaacc ttgatgaggt cgtctgcagt ggctctcgc ttcataccgc	60
tnccatcgtc atactgtagg ttgcccacca cytctgggca tcttggggcg gcntaatatt	120
ccaggaaact ctcaatcaag tcaccgtcga tgaaacctgt gggctgggtc tgtcttcgc	180
tcggtgtgaa aggatctccc agaaggagtg ctcgatcttc cccacacttt tgatgacttt	240
attgagtcga ttctgcatgt ccagcaggag gttgtaccag ctctctgaca gtgaggtcac	300
cagccctatc atgcggttga mcgtgccgaa garcaccgag ccttggtgtg gggkkgagt	360
ctcaccacaga ttctgcatta ccagagagcc gtggcaaaag acattgacaa actcgcccag	420
gtggaaaaag amcamctcct ggargtgctn gccgctctc gtcmgtttgt ggcagcgctw	480

```
tccttttgac acacaaacaa gttaaaggca ttttcagccc ccagaaantt gtcatcatcc 540
aagatntcgc acagcactna tccagttggg attaaat 577
```

<210> 187

<211> 534

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(534)

<223> n = A,T,C or G

<400> 187

```
aacatcttcc tgtataatgc tgtgtaatat cgatccgatn ttgtctgstg agaatycatw 60
actkggaaaa gmaacattaa agcctggaca ctggtattaa aattcacat atgcaacact 120
ttaaacagtg tgtcaatctg ctcccyynac ttgtcatca ccagtctggg aakaagggtta 180
tgccctattc acacctgtta aaagggcgct aagcattttt gattcaacat cttttttttt 240
gacacaagtc cgaaaaaagc aaaagtaaac agttatyaat ttgttagcca attcactttc 300
ttcatgggac agagccatyt gatttaaaaa gcaaattgca taatattgag ctttygggagc 360
tgatatttga gcggaagagt agcctttcta cttcaccaga cacaactccc ttcatattg 420
ggatgttnac naaagtwatg tctctwacag atgggatgct tttgtggcaa ttctgttctg 480
aggatctccc agtttattta ccacttgcac aagaaggcgt tttcttcctc aggc 534
```

<210> 188

<211> 761

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(761)

<223> n = A,T,C or G

<400> 188

```
agaaaccagt atctctnaaa acaacctctc ataccttggt gacctaatth tgtgtgcgtg 60
tgtgtgtgcg cgcataattat atagacaggc acatcttttt tacttttgta aaagcttatg 120
cctcttttgg atctatatct gtgaaagtth taatgatctg ccataatgct ttggggacct 180
ttgtcttctg tgtaaatggt actagagaaa acacctatnt tatgagtcac tctagttngt 240
tttattcgac atgaaggaaa tttccagatn acaacactna caaactctcc ctkgackarg 300
ggggacaaaag aaaagcaaaa ctgamcataa raaacaatwa cctgggtgaga arttgcataa 360
acagaaatwr ggtagtatat tgaarnacag catcattaaa rmgttwtktt wttctccctt 420
gcaaaaaaca tgtaacngact tcccgttgag taatgccaaag ttgttttttt tatnataaaa 480
cttgcccttc attacatgtt tnaaagtggg gtgggtgggc aaaatattga aatgatggaa 540
ctgactgata aagctgtaca aataagcagt gtgcctaaca agcaacacag taatgttgac 600
atgcttaatt cacaaatgct aatttcatta taaatgtttg ctaaaataca ctttgaacta 660
ttttctgtgn ttcccagagc tgagatntta gattttatgt agtatnaagt gaaaaantac 720
gaaaataata acattgaaga aaananaaaa aaanaaaaaa a 761
```

<210> 189

<211> 482

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(482)

<223> n = A,T,C or G

```

<400> 189
tttttttttt tttgccgatn ctactatattt attgcaggan gtgggggtgt atgcaccgca      60
caccggggct atnagaagca agaaggaagg agggagggca cagccccttg ctgagcaaca      120
aagccgctgt ctgccttctc tgtctgtctc ctgggtgcagg cacatgggga gaccttcccc      180
aaggcagggg ccaccagtcc aggggtggga atacaggggg tgggagtgt gcataagaag      240
tgataggcac aggccacccg gtacagaccc ctcggtctct gacaggtnga tttcgaccag      300
gtcattgtgc cctgcccagg cacagcgtan atctggaaaa gacagaatgc tttccttttc      360
aaatttggtc ngtcatngaa ngggcanttt tccaanttng gctnngtctt ggtacncttg      420
gttcggccca gctcncgctc caaaaantat tcaccennct ccnaattgct tgcnggnccc      480
cc

```

<210> 190

<211> 471

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(471)

<223> n = A,T,C or G

```

<400> 190
tttttttttt ttttaaaaca gtttttcaca aaaaaattta ttagaagaat agtggttttg      60
aaaactctcg catccagtga gaactacat acaccacatt acagctngga atgtntcca      120
aatgtctggt caaatgatac aatggaacca ttcaatctta cacatgcacg aaagaacaag      180
cgcttttgac atacaatgca caaaaaaaaa aggggggggg gaccacatgg attaaaattt      240
taagtactca tcacatacat taagacacag ttctagtcca gtcnaaaatc agaactgcnt      300
tgaaaaattt catgtatgca atccaaccaa agaacttnat tggatgatcat gantnctcta      360
ctacatcnac cttgatcatt gccaggaacn aaaagttnaa ancacncngt acaaaaaanaa      420
tctgtaattn anttcaacct ccgtacngaa aaatnttntt tatacactoc c              471

```

<210> 191

<211> 402

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(402)

<223> n = A,T,C or G

```

<400> 191
gagggattga aggtctgttc tastgtcggm ctgttcagcc accaactcta acaagttgct      60
gtcttccact cactgtctgt aagcttttta acccagacwg tatcttcata aatagaacaa      120
attcttcacc agtcacatct tctaggacct ttttggtatc agttagtata agctcttcca      180
cttcctttgt taagacttca tctggtaaag tcttaagttt ttagaaaagg aattyaattg      240
ctcgttctct aacaatgtcc tctccttgaa gtatttggtc gaacaacca cctaaagtcc      300
ctttgtgcat ccattttaaa tatacttaat agggcattgk tncactaggt taaattctgc      360
aagagtcata tgtctgcaaa agttgcgtta gtatatctgc ca              402

```

<210> 192

<211> 601

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(601)

<223> n = A,T,C or G

<400> 192

gagctcggat	ccaataatct	ttgtctgagg	gcagcacaca	tatncagtgc	catggnaact	60
ggtctacccc	acatgggagc	agcatgccgt	agntatataa	ggtcattccc	tgagtcagac	120
atgcytyttt	gaytaccgtg	tgccaagtgc	tggtgattct	yaacacacyt	ccatcccgyt	180
cttttgtgga	aaaactggca	cttkcttgga	actagcarga	catcacttac	aaattcaccc	240
acgagacact	tgaaagggtg	aacaaagcga	ytcttgcat	gctttttgtc	cctccggcac	300
cagttgtcaa	tactaaccgc	ctggtttgcc	tccatcacat	ttgtgatctg	tagctctgga	360
tacatctcct	gacagtactg	aagaacttct	tcttttgttt	caaaagcarg	tcttggtgcc	420
tggttgatca	ggttcccat	tcccagtcyg	aatgttcaca	tggtcatatt	wacttccac	480
aaaacattgc	gatttgaggc	tcagcaacag	caaatcctgt	tccggcattg	gctgcaagag	540
cctcgatgta	gccggccagc	gccaaggcag	gcgccgtgag	ccccaccagc	agcagaagca	600
g						601

<210> 193

<211> 608

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(608)

<223> n = A,T,C or G

<400> 193

atacagccca	nateccacca	cgaagatgcg	cttggtgact	gagaacctga	tgcggtcact	60
ggtcccgtcg	tagccccagc	gactctccac	ctgctggaag	cggttgatgc	tgactctytt	120
cccaacgcag	gcagmagcgg	gscgggtcaa	tgaactccay	tcgtggcttg	gggtkgacgg	180
tkaagtgcag	gaagaggctg	accacctcgc	ggtccaccag	gatgcccgac	tgtagcgggac	240
ctgcagcgaa	actcctcgat	ggtcatgagc	gggaagcgaa	tgaggcccag	ggccttgccc	300
agaaccttcc	gcctgttctc	tggcgtcacc	tgacgtgctc	gccgctgava	ctcggcctcg	360
gaccagcgga	caaacggcrt	tgaacagccg	cacctcacgg	atgccagtg	tgtagcgctc	420
caggammgsc	accagcgtgt	ccagggtcaat	gtcggtgaag	ccctcccgcg	gtrattggcgt	480
ctgcagtggt	tttgcgatg	ttctccaggc	acaggctggc	cagctgcggg	tcacgaaga	540
gtcgcgctcg	cgtgagcagc	atgaaggcgt	tgtaggctcg	cagttcttct	tcagggaactc	600
cacgcaat						608

<210> 194

<211> 392

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(392)

<223> n = A,T,C or G

<400> 194

gaacggctgg	accttgccctc	gcattgtgct	tgctggcagg	gaataccttg	gcaagcagyt	60
ccagtcgag	cagccccaga	ccgctgccgc	ccgaagctaa	gcctgcctct	ggccttcccc	120
tccgcctcaa	tgacgaacca	gtagtgggag	cactgtgttt	agagttaaga	gtgaacactg	180
tttgatttta	cttggaatt	tctctgttta	tatagctttt	cccaatgcta	atttccaaac	240
aacaacaaca	aaataacatg	tttgccctgtt	aagttgtata	aaagtaggtg	attctgtatt	300
taaagaaaat	attactgtta	catatactgc	ttgcaatttc	tgtatttatt	gktinctstgg	360
aaataaatat	agttattaaa	ggttgctcant	cc			392

<210> 195
 <211> 502
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(502)
 <223> n = A,T,C or G

<400> 195
 ccsttkgagg ggtkaggkyc cagtttyccga gtggaagaaa caggccagga gaagtgcgtg 60
 ccgagctgag gcagatgttc ccacagtgc cccagagacc stgggstata gtytctgacc 120
 cctcncaagg aaagaccacs ttctggggac atgggctgga gggcaggacc tagaggcacc 180
 aagggaaggc ccatttccgg ggstgttccc cgaggaggaa gggaaggggc tctgtgtgcc 240
 ccccasgagg aagaggccct gagtctgtgg atcagacacc ccttcacgtg tatccccaca 300
 caaatgcaag ctcaccaagg tcccctctca gtccccttcc stacaccctg amcggccact 360
 gscscacacc caccagagc acgccaccg ccatggggar tgtgctcaag gartcgcnng 420
 gcarcgtgga catctngtcc cagaaggggg cagaatctcc aatagangga ctgarcmstt 480
 gctnanaaaa aaaaanaaaa aa 502

<210> 196
 <211> 665
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(665)
 <223> n = A,T,C or G

<400> 196
 ggttacttgg tttcattgcc accacttagt ggatgtcatt tagaaccatt ttgtctgctc 60
 cctctggaag ccttgcgag agcggacttt gtaattgttg gagaataact gctgaatttt 120
 wagctgtttk gagttgatts gcaccactgc acccacaact tcaatatgaa aacyawttga 180
 actwatttat tatcttgtga aaagtataac aatgaaaatt ttgttcatac tgtattkac 240
 aagtatgatg aaaagcaawa gatatatatt cttttattat gttaaattat gattgccatt 300
 attaatcggc aaaatgtgga gtgtatgttc ttttcacagt aatatatgcc ttttgtaact 360
 tcacttggtt attttattgt aaatgartta caaaattctt aatttaagar aatggtatgt 420
 watatttatt tcattaattt ctttcctkgt ttacgtwaat ttgaaaaga wtgcatgatt 480
 tcttgacaga aatcgatctt gatgctgtgg aagtagtttg acccacatcc ctatgagttt 540
 ttcttagaat gtataaagggt tgtagcccat cnaacttcaa agaaaaaat gaccacatcc 600
 tttgcaatca ggctgaaatg tggcatgctn ttctaattcc aactttataa actagcaaan 660
 aagtg 665

<210> 197
 <211> 492
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(492)
 <223> n = A,T,C or G

<400> 197
 tttntttttt ttttttttgc aggaaggatt ccatttattg tggatgcatt ttcacaatat 60
 atgtttattg gagcgatcca ttatcagtga aaagtatcaa gtgtttataa natttttagg 120

```

aaggcagatt cacagaacat gctngtcngc ttgcagtttt acctcgtana gatnacagag      180
aatttatagtc naaccagtaa acnaggaatt tacttttcaa aagattaaat ccaaactgaa      240
caaaaattcta ccctgaaact tactccatcc aaatatgga ataanagtca gcagtgatac      300
attctcttct gaactttaga tttctagaa aaatatgtaa tagtgatcag gaagagctct      360
tgttcaaaag tacaacnaag caatgttccc ttaccatagg ccttaattca aactttgatc      420
catttcactc ccatcacggg agtcaatgct acctgggaca cttgtatttt gttcatnctg      480
ancntggctt aa                                         492

```

<210> 198

<211> 478

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(478)

<223> n = A,T,C or G

<400> 198

```

ttnttttgn atttcantct gtannaanta ttttcattat gtttattana aaaatatnaa      60
tgtntccacn acaaatcatn ttacntnagt aagaggccan ctacattgta caacatacac      120
tgagtatatt ttgaaaagga caagtttaaa gtanacncat attgccganc atancacatt      180
tatacatggc ttgattgata tttagcacag canaaactga gtgagttacc agaaanaaat      240
natatatgtc aatcngattt aagatacaaa acagatccta tggtagatan catcntgtag      300
gagttgtggc tttatgttta ctgaaagtca atgcagttcc tgtacaaaga gatggccgta      360
agcattctag tacctctact ccatggttaa gaatcgtaca cttatgttta catatgtnc      420
gggtaagaat tgtgttaagt naanttatgg agaggtccan gagaaaaatt tgatncaa      478

```

<210> 199

<211> 482

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(482)

<223> n = A,T,C or G

<400> 199

```

agtgacttgt cctccaacaa aacccttga tcaagtttgt ggcactgaca atcagaccta      60
tgctagtctc tgtcatctat tcgtacttaa atgcagactg gaggggacca aaaaggggca      120
tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga      180
agtgattcag tttcctctac ggatgagaga ctggctcaag aatatcctca tgcagcttta      240
tgaagccnac tctgaacacg ctggttatct nagatgagaa ncagagaaat aaagtcnaga      300
aaatttacct ggangaaaag aggccttngg ctggggacca tccattgaa ccttctctta      360
anggacttta agaanaaact accacatgtn tgtngtatcc tgggtgccngg ccgtttantg      420
aacntngacn ncacccttnt ggaatanant cttgacngcn tcctgaactt gtcctctg      480
ga

```

<210> 200

<211> 270

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(270)

<223> n = A,T,C or G

```

<400> 200
cggccgcaag tgcaactcca gctggggccg tgcggacgaa gattctgcca gcagttggtc      60
cgactgcgac gacggcggcg gcgacagtcg caggtgcagc gcgggcgcct ggggtcttgc      120
aaggctgagc tgacgccgca gaggtcgtgt cacgtcccac gaccttgacg ccgtcgggga      180
cagccggaac agagcccgtt gaangcggga ggcctcgggg agccctcggg gaagggcggc      240
ccgagagata cgcaggtgca ggtggccgcc                                     270

```

```

<210> 201
<211> 419
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(419)
<223> n = A,T,C or G

```

```

<400> 201
tttttttttt ttttggaaatc tactgcgagc acagcaggtc agcaacaagt ttatttttgc      60
gctagcaagg taacagggtg gggcatgggt acatgttcag gtcaacttcc tttgtcgtgg      120
ttgattgggt tgtctttatg ggggcggggt ggggtagggg aaancgaagc anaantaaca      180
tggagtgggt gcacctccc tgtagaacct ggttacnaaa gcttggggca gttcacctgg      240
tctgtgacgg tcattttctt gacatcaatg ttattagaag tcaggatata ttttagagag      300
tccactgtnt ctggaggagg attagggttt cttgccanaa tccaancaaa atccacntga      360
aaaagttgga tgatncangt acngaatacc ganggcatan ttctcatant cggtggcca      419

```

```

<210> 202
<211> 509
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(509)
<223> n = A,T,C or G

```

```

<400> 202
tttntttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt      60
tggcacttaa tccattttta tttcaaaatg tctacaaant ttnaatncnc cattatacng      120
gtnattttnc aaaatctaaa nnttattcaa attnnagcca aantccttac ncaaattnaa      180
tacnncnaaa aatcaaaaat atacntntct ttcagcaaac ttngttacat aaattaaaaa      240
aatatatacg gctgggtgtt tcaaagtaca attatcttaa cactgcaaac atnttttnaa      300
ggaactaaaa taataaaaaa cactnccgca aagggttaaag ggaacaacaa attcntttta      360
caacancnnc nattataaaa atcatatctc aaatccttagg ggaatatata cttcacacng      420
ggatcttaac ttttactnca ctttgtttat ttttttanaa ccattgtntt gggcccaaca      480
caatggnaat nccnccnccn tggactagt                                     509

```

```

<210> 203
<211> 583
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(583)
<223> n = A,T,C or G

```



```

<400> 203
tttttttttt ttttttttga cccccctctt ataaaaaaca agttaccatt ttatttttact    60
tacacatatt ttttttataa ttggtattag atattcaaaa ggcagctttt aaaatcaaac    120
taaatggaaa ctgccttaga tacataattc ttaggaatta gcttaaaatc tgcctaaagt    180
gaaaaatcttc tctagctctt ttgactgtaa atttttgact cttgtaaaaac atccaaattc    240
atttttcttg tctttaaaat tatctaattc ttccattttt tccctattcc aagtcaattt    300
gcttctctag cctcatttcc tagctcttat ctactattag taagtggcct ttttctctaa    360
agggaaaaaca ggaagagana atggcacaca aaacaaacat tttatattca tatttctacc    420
tacgttaata aaatagcatt ttgtgaagcc agctcaaaaag aaggcttaga tccttttatg    480
tccatttttag tcactaaacg atatcnaaag tgccagaatg caaaagggtt gtgaacattt    540
attcaaaagc taatataaga tatttcacat actcatcttt ctg                    583

```

<210> 204

<211> 589

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(589)

<223> n = A,T,C or G

```

<400> 204
ttttttttnt tttttttttt ttttttnctc ttcttttttt ttganaatga ggatcgagtt    60
tttcaacttc tagatagggc atgaagaaaa ctcatctttc cagcttttaa ataacaatca    120
aatctcttat gctatatcat attttaagtt aaactaatga gtcactggct tatcttctcc    180
tgaaggaaat ctgttcattc ttctcattca tatagttata tcaagtacta ccttgcatat    240
tgagagggtt ttcttctcta ttacacata tatttccatg tgaatttgta tcaaaccctt    300
attttcatgc aaactagaaa ataatgtntt cttttgcata agagaagaga acaatatnag    360
cattacaaaa ctgctcaaat tgtttggtta gnntatccat tataattagt tnggcaggag    420
ctaatacaaa tcacatttac ngacnagcaa taataaaaact gaagtaccag ttaaatatcc    480
aaaataatta aaggaacatt tttagcctgg gtataattag ctaattcact ttacaagcat    540
ttattnagaa tgaattcaca tgttattatt cnttagccca acacaatgg                    589

```

<210> 205

<211> 545

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(545)

<223> n = A,T,C or G

```

<400> 205
ttttnttttt ttttttcagt aataatcaga acaatattta tttttatatt taaaattcat    60
agaaaagtgc cttacattta ataaaagttt gtttctcaaa gtgatcagag gaattagata    120
tngtcttgaa caccaatatt aatttgagga aaatacacca aaatacatta agtaaattat    180
ttaagatcat agagcttgta agtgaagaaga taaaatttga cctcagaaac tctgagcatt    240
aaaaatccac tattagcaaa taaattacta tggacttctt gctttaattt tgtgatgaat    300
atgggggtgc actggtaaac caacacattc tgaaggatac attacttagt gatagattct    360
tatgtacttt gctanatnac gtggatatga gttgacaagt ttctctttct tcaatctttt    420
aaggggcnag ngaaatgagg aagaaaagaa aaggattacg catactgttc tttctatnng    480
aaggattaga tatgtttcct ttgccaatat taaaaaata ataattgtta ctactagtga    540
aacc                    545

```

<210> 206

<211> 487

<212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(487)
 <223> n = A,T,C or G

<400> 206
 tttttttttt ttttttagtc aagtttctna tttttattat aattaaagtc ttggtcattt 60
 catttattag ctctgcaact tacatattta aattaaagaa acgttnttag acaactgtna 120
 caatttataa atgtaagggtg ccattattga gtanatatat tcctccaaga gtggatgtgt 180
 cccttctccc accaactaat gaancagcaa cattagttaa attttatttag tagatnatac 240
 actgctgcaa acgctaattc tcttctccat ccccatgtng atattgtgta tatgtgtgag 300
 ttggttagaa tgcatacanca atctnacaat caacagcaag atgaagctag gcntgggctt 360
 tcggtgaaaa tagactgtgt ctgtctgaat caaatgatct gacctatcct cgggtggcaag 420
 aactcttcga accgcttcct caaaggcngc tgccacattt gtggcntctn ttgcacttgt 480
 ttcaaaa 487

<210> 207
 <211> 332
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(332)
 <223> n = A,T,C or G

<400> 207
 tgaattggct aaaagactgc atttttanaa ctagcaactc ttatttcttt cctttaaaaa 60
 tacatagcat taaatcccaa atcctattta aagacctgac agcttgagaa ggtcactact 120
 gcatttataa gaccttctgg tggttctgct gttacntttg aantctgaca atccttgana 180
 atctttgcat gcagaggagg taaaagggtat tggattttca cagaggaana acacagcgca 240
 gaaatgaagg ggccaggctt actgagcttg tccactggag ggctcatggg tgggacatgg 300
 aaaagaaggc agcctaggcc ctggggagcc ca 332

<210> 208
 <211> 524
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(524)
 <223> n = A,T,C or G

<400> 208
 agggcgtggt gcggaggcg tttactgttt gtctcagtaa caataaatac aaaaagactg 60
 gttgtgttcc ggcctcatcc aaccacgaag ttgatttctc ttgtgtgcag agtgactgat 120
 tttaaaggac atggagcttg tcacaatgtc acaatgtcac agtgtgaagg gcacactcac 180
 tcccgcgtga ttcacattta gcaaccaaca atagctcatg agtccatact tgtaataact 240
 tttggcagaa tacttnttga aacttgaga tgataactaa gatccaagat atttcccaaa 300
 gtaaatagaa gtgggtcata atattaatta cctgttcaca tcagcttcca ttacaagtc 360
 atgagcccag aactgacat caaactaagc ccacttagac tcctcaccac cagtctgtcc 420
 tgtatcaga caggaggctg tcaccttgac caaattctca ccagtcaatc atctatccaa 480
 aaaccattac ctgatccact tccggtaatg caccaccttg gtga 524

<210> 209
 <211> 159
 <212> DNA
 <213> Homo sapien

<400> 209
 ggggtgaggaa atccagagtt gccatggaga aaattccagt gtcagcattc ttgtctccttg 60
 tggccctctc ctacactctg gccagagata ccacagtcaa acctggagcc aaaaaggaca 120
 caaaggactc tcgacccaaa ctgccccaga ccctctcca 159

<210> 210
 <211> 256
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(256)
 <223> n = A,T,C or G

<400> 210
 actccctggc agacaaaggc agaggagaga gctctgttag ttctgtgttg ttgaactgcc 60
 actgaatttc tttccacttg gactattaca tgccanttga gggactaatg gaaaaacgta 120
 tggggagatt ttanccaatt tangtntgta aatggggaga ctggggcagg cgggagagat 180
 ttgcaggggtg naaatgggan ggctgggttg ttanatgaac agggacatag gaggtaggca 240
 ccaggatgct aaatca 256

<210> 211
 <211> 264
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(264)
 <223> n = A,T,C or G

<400> 211
 acattgtttt tttgagataa agcattgaga gagctctcct taacgtgaca caatggaagg 60
 actggaacac atacccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt 120
 atattcaagc acatatgtta tatattattc agttccatgt ttatagccta gttaaggaga 180
 ggggagatac attcngaaag aggactgaaa gaaatactca agtnggaaaa cagaaaaaga 240
 aaaaaaggag caaatgagaa gcct 264

<210> 212
 <211> 328
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(328)
 <223> n = A,T,C or G

<400> 212
 acccaaaaat ccaatgctga atatttggtc tcattattcc canattcttt gattgtcaaa 60
 ggatttaatg ttgtctcagc ttgggcactt cagttaggac ctaaggatgc cagccggcag 120
 gtttatatat gcagcaacaa tattcaagcg cgacaacagg ttattgaact tgcccgccag 180

ttnaatttca	ttccattga	cttgggatcc	ttatcatcag	ccagagagat	tgaaaattta	240
cccctacnac	tctttactct	ctgganaggg	ccagtgggtg	tagctataag	cttggccaca	300
tttttttttc	ctttattcct	ttgtcaga				328

<210> 213

<211> 250

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (250)

<223> n = A,T,C or G

<400> 213

acttatgagc	agagcgacat	atccnagtgt	agactgaata	aaactgaatt	ctctccagtt	60
taaagcattg	ctcactgaag	ggatagaagt	gactgccagg	agggaaagta	agccaaggct	120
cattatgccca	aagganatat	acatttcaat	tctccaaact	tcttcctcat	tccaagagtt	180
ttcaatatatt	gcatgaacct	gctgataanc	catgttaana	aacaaatata	tctctnacct	240
tctcatcggt						250

<210> 214

<211> 444

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (444)

<223> n = A,T,C or G

<400> 214

accagaatc	caatgctgaa	tatttggtt	cattattccc	agattctttg	attgtcaaag	60
gatttaagt	tgtctcagct	tgggcacttc	agttaggacc	taaggatgcc	agccggcagg	120
tttatatatg	cagcaacaat	attcaagcgc	gacaacagg	tattgaactt	gcccgccagt	180
tgaatttcat	tcccattgac	ttgggatcct	tatcatcagc	canagagatt	gaaaatttac	240
ccctacgact	ctttactctc	tggagagggc	cagtgggtgt	agctataagc	ttggccacat	300
ttttttttcc	tttattcctt	tgtcagagat	gcgattcacc	catatgctan	aaaccaacag	360
agtgaacttt	acaaaattcc	tataganatt	gtgaataaaa	ccttacctat	agttgccatt	420
actttgctct	ccctaataata	cctc				444

<210> 215

<211> 366

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (366)

<223> n = A,T,C or G

<400> 215

acttatgagc	agagcgacat	atccaagtgt	anactgaata	aaactgaatt	ctctccagtt	60
taaagcattg	ctcactgaag	ggatagaagt	gactgccagg	agggaaagta	agccaaggct	120
cattatgccca	aagganatat	acatttcaat	tctccaaact	tcttcctcat	tccaagagtt	180
ttcaatatatt	gcatgaacct	gctgataagc	catgttgaga	aacaaatata	tctctgacct	240
tctcatcggt	aagcagaggc	tgtaggcaac	atggaccata	gcgaanaaaa	aacttagtaa	300
tccaagctgt	tttctacact	gtaaccagg	ttccaaccaa	ggtggaaatc	tcctatactt	360

ggtgcc

366

<210> 216
 <211> 260
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(260)
 <223> n = A,T,C or G

<400> 216
 ctgtataaac agaactccac tgcangaggg agggccgggc caggagaatc tccgcttgtc 60
 caagacaggg gcctaaggag ggtctccaca ctgctnntaa gggctnttnc atttttttat 120
 taataaaaag tnnaaaaggc ctcttctcaa cttttttccc ttnggctgga aaatttataa 180
 atcaaaaatt tccnaagtt ntcaagctat catatatact ntatcctgaa aaagcaacat 240
 aattcttctt tccctccttt 260

<210> 217
 <211> 262
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(262)
 <223> n = A,T,C or G

<400> 217
 acctacgtgg gtaagtttan aaatgttata atttcaggaa naggaacgca tataattgta 60
 tcttgcttat aattttctat ttttaataagg aaatagcaaa ttgggggtggg gggaatgtag 120
 ggcattctac agtttgagca aaatgcaatt aaatgtggaa ggacagcact gaaaaatttt 180
 atgaataatc tgtatgatta tatgtctcta gagtagattt ataattagcc acttacccta 240
 atatccttca tgcttgtaaa gt 262

<210> 218
 <211> 205
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(205)
 <223> n = A,T,C or G

<400> 218
 accaaggtgg tgcattaccg gaantggatc aangacacca tcgtggccaa cccctgagca 60
 cccctatcaa ctcccttttg tagtaaacctt ggaaccttgg aaatgaccag gccaaagactc 120
 aggcctcccc agttctactg acctttgtcc ttangtntna ngtcacagggt tgctaggaaa 180
 anaaatcagc agacacaggt gtaaa 205

<210> 219
 <211> 114
 <212> DNA
 <213> Homo sapien

<400> 219

tactgttttg tctcagtaac aataaatata aaaagactgg ttgtgttccg gccccatcca 60
accacgaagt tgatttctct tgtgtgcaga gtgactgatt ttaaaggaca tgga 114

<210> 220
<211> 93
<212> DNA
<213> Homo sapien

<400> 220
actagccagc acaaaaaggca gggtagcctg aattgctttc tgctctttac atttctttta 60
aaataagcat ttagtgctca gtccctactg agt 93

<210> 221
<211> 167
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(167)
<223> n = A,T,C or G

<400> 221
actangtgca ggtgcgacaca aatatttgtc gatattccct tcatcttga ttccatgagg 60
tcttttgccc agcctgtggc tctactgtag taagtttctg ctgatgagga gccagnatgc 120
ccccactac cttccctgac gtcceccana aatcacccaa cctctgt 167

<210> 222
<211> 351
<212> DNA
<213> Homo sapien

<400> 222
agggcgtggt gcggagggcg gtactgacct cattagtagg aggatgcatt ctggcacccc 60
gttcttcacc tgtccccaa tccttaaaag gccatactgc ataaagtcaa caacagataa 120
atgtttgctg aattaaagga tggatgaaaa aaattaataa tgaatttttg cataatccaa 180
ttttctcttt tatatttcta gaagaagttt ctttgagcct attagatccc gggaatcttt 240
taggtgagca tgattagaga gcttgtagggt tgcttttaca tatatctggc atatttgagt 300
ctcgatatcaa aacaatagat tggtaaagggt ggtattattg tattgataag t 351

<210> 223
<211> 383
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(383)
<223> n = A,T,C or G

<400> 223
aaaacaaca acaaaaaaaa acaattcttc attcagaaaa attatcttag ggactgatat 60
tggtattat ggtaattta atwrtrttkt ggggcatttc cttacattgt cttgacaaga 120
ttaaaatgtc tgtgccaaaa ttttgtattt tatttggaga cttcttatca aaagtaatgc 180
tgccaaagga agtctaagga attagtagtg ttcccmcac ttgtttggag tgtgctattc 240
taaaagattt tgatttcctg gaatgacaat tatattttta ctttgggtggg ggaaanagtt 300
ataggaccac agtcttcact tctgatactt gtaaattaat cttttattgc acttgttttg 360
accattaagc tatatgttta aaa 383

<210> 224
 <211> 320
 <212> DNA
 <213> Homo sapien

<400> 224
 cccctgaagg cttcttggtta gaaaatagta cagttacaac caataggaac aacaaaaaga 60
 aaaagtttgt gacattgtag tagggagtggt gtacccttta ctcccatca aaaaaaaaaat 120
 ggatacatgg ttaaaggata raagggcaat attttatcat atgttctaaa agagaaggaa 180
 gagaaaatac tactttctcr aaatggaagc ccttaaagggt gctttgatac tgaaggacac 240
 aaatgtgggc gtccatcctc ctttaragtt gcatgacttg gacacggtaa ctgttgacagt 300
 ttaractcm gcattgtgac 320

<210> 225
 <211> 1214
 <212> DNA
 <213> Homo sapien

<400> 225
 gaggactgca gcccgcactc gcagccctgg caggcggcac tggtcatgga aaacgaattg 60
 ttctgctcgg gcgtcctggt gcacccgcag tgggtgctgt cagccgcaca ctgtttccag 120
 aactcctaca ccacggggtt gggcctgcac agtcttgagg ccgaccaaga gccaggagagc 180
 cagatggtgg aggccagcct ctccgtacgg caccagaggt acaacagacc cttgctcgct 240
 aacgacctca tgctcatcaa gttggacgaa tccgtgtccg agtctgacac catccggagc 300
 atcagcattg cttcgagtg ccctaccgcg gggaactctt gctcgtttc tggctgggggt 360
 ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg tgaacgtgtc ggtggtgtct 420
 gaggaggtct gcagtaagct ctatgacctg ctgtaccacc ccagcatggt ctgcgccggc 480
 ggagggcaag accagaagga ctctgcaaac ggtgactctg gggggccctt gatctgcaac 540
 gggtaacttg agggccttgt gtctttcgga aaagccccgt gtggccaagt tggcgtgcca 600
 ggtgtctaca ccaacctctg caaattcact gagtggatag agaaaaccgt ccaggccagt 660
 taactctggg gactgggaac ccattgaaatt gacccccaaa tacatcctgc ggaaggaaatt 720
 caggaatatc tgttcccagc ccctcctccc tcaggcccag gagtccaggc cccagcccc 780
 tcctcctca aaccaagggt acagatcccc agcccctcct ccctcagacc caggagtcca 840
 gacccccag ccctcctcc ctcagaccca ggagtccagc ccctcctccc tcagaccag 900
 gagtccagac ccccagccc ctctcctcc agaccagggt gtccaggccc ccaaccctc 960
 ctccctcaga ctcagaggtc caagccccca acccctcctt cccagacccc agaggtccag 1020
 gtcccagccc ctctcctcc agacccagcg gtccaatgcc acctagactc tcctgtaca 1080
 cagtgcctcc ttgtggcacg ttgacccaac cttaccagtt ggtttttcat ttttgtccc 1140
 tttccctag atccagaaat aaagtctaag agaagcgcaa aaaaaaaaaa aaaaaaaaaa 1200
 aaaaaaaaaa aaaa 1214

<210> 226
 <211> 119
 <212> DNA
 <213> Homo sapien

<400> 226
 acccagtatg tgcagggaga cggaacccca tgtgacagcc cactccacca gggttcccaa 60
 agaacctggc ccagtcataa tcattcatcc tgacagtggc aataatcacg ataaccagt 119

<210> 227
 <211> 818
 <212> DNA
 <213> Homo sapien

<400> 227
 acaattcata gggacgacca atgaggacag ggaatgaacc cggtctctcc ccagccctga 60

tttttgetac	atatgggggtc	ccttttcatt	ctttgcaaaa	acactggggtt	ttctgagaac	120
acggacgggt	cttagcacia	tttgtgaaat	ctgtgtaraa	cggggctttg	caggggagat	180
aattttcttc	ctctggagga	aaggtgggtga	ttgacaggca	gggagacagt	gacaaggcta	240
gagaaagcca	cgctcggcct	tctctgaacc	aggatggaa	ggcagacccc	tgaaaacgaa	300
gcttgtcccc	ttccaatcag	ccacttctga	gaaccccat	ctaacttctt	actggaaaag	360
agggcctcct	caggagcagt	ccaagagttt	tcaaagataa	cgtgacaact	accatctaga	420
ggaaaggggt	caccctcagc	agagaagccg	agagcttaac	tctggtcggt	tccagagaca	480
acctgctggc	tgtcttggga	tgcgccagc	ctttgagagg	ccactacccc	atgaacttct	540
gccatccact	ggacatgaag	ctgaggacac	tgggcttcaa	cactgagttg	tcatgagagg	600
gacaggctct	gccctcaagc	cggctgaggg	cagcaaccac	tctcctcccc	tttctcacgc	660
aaagccattc	ccacaaatcc	agaccatacc	atgaagcaac	gagacccaaa	cagtttggct	720
caagaggata	tgaggactgt	ctcagcctgg	ctttgggctg	acaccatgca	cacacacaag	780
gtccacttct	aggttttcag	cctagatggg	agtcgtgt			818

<210> 228

<211> 744

<212> DNA

<213> Homo sapien

<400> 228

actggagaca	ctgttgaact	tgatcaagac	ccagaccacc	ccaggtctcc	ttcgtgggat	60
gtcatgacgt	ttgacatacc	tttggaacga	gcctcctcct	tgggaagatgg	aagaccgtgt	120
tctgtggccga	cctggcctct	cctggcctgt	ttcttaagat	gaggagtcac	atttcaatgg	180
taggaaaagt	ggcttcgtaa	aatagaagag	cagtcactgt	ggaactacca	aatggcgaga	240
tgctcgggtc	acattggggg	gctttgggat	aaaagattta	tgagccaact	attctctggc	300
accagattct	aggccagttt	gttccactga	agcttttccc	acagcagtc	acctctgcag	360
gctggcagct	gaatggcttg	cgggtgggtc	tgtggcaaga	tcacactgag	atcgatgggt	420
gagaaggcta	ggatgcttgt	ctagtgttct	tagctgtcac	gttggctcct	tccaggttgg	480
ccagacgggt	ttggccactc	ccttctaaaa	cacaggcgcc	ctcctgggtga	cagtgaacct	540
ccgtgggtat	ccttggccca	ttccagcagt	cccagttatg	catttcaagt	ttgggggttg	600
ttcttttctg	taatgttctt	ctgtgttctc	agctgtcttc	atttctctgg	ctaagcagca	660
ttgggagatg	tggaccagag	atccactcct	taagaaccag	tggcgaaaga	cactttcttt	720
cttcactctg	aagtagctgg	tggt				744

<210> 229

<211> 300

<212> DNA

<213> Homo sapien

<400> 229

cgagtctggg	ttttgtctat	aaagtttgat	ccctcctttt	ctcatccaaa	tcatgtgaac	60
cattacacat	cgaaataaaa	gaaaggtggc	agacttgccc	aacgccaggc	tgacatgtgc	120
tgagggttg	ttgtttttta	attattattg	ttagaaacgt	caccacagct	ccctgttaat	180
ttgtatgtga	cagccaactc	tgagaaggtc	ctatttttcc	acctgcagag	gatccagctc	240
cactaggctc	ctccttgccc	tcacactgga	gtctccgcca	gtgtgggtgc	ccactgacat	300

<210> 230

<211> 301

<212> DNA

<213> Homo sapien

<400> 230

cagcagaaca	aatacaaaata	tgaagagtgc	aaagatctca	taaaatctat	gctgaggaat	60
gagcgacagt	tcaaggagga	gaagcttgca	gagcagctca	agcaagctga	ggagctcagg	120
caatataaag	tcttggttca	cactcaggaa	cgagagctga	cccagtttaag	ggagaagtgg	180
cgggaaggga	gagatgcctc	cctctcattg	aatgagcatc	tccaggccct	cctcactccg	240
gatgaaccgg	acaagtccca	ggggcaggac	ctccaagaaa	cagacctcgg	ccgcgaccac	300
g						301

<210> 231
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 231
 gcaagcagc tggcaaactct ctgtcaggtc agctccagag aagccattag tcatttttagc 60
 caggaactcc aagtccacat ccttggaac tggggacttg cgcaggttag ccttgaggat 120
 ggcaacacgg gactttctcat caggaagtgg gatgtagatg agctgatcaa gacggccagg 180
 tctgaggatg gcaggatcaa tgatgtcagg ccggttggtta ccgccaatga tgaacacatt 240
 tttttttgtg gacatgccat ccattttctgt caggatctgg ttgatgactc ggtcagcagc 300
 c 301

<210> 232
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 232
 agtaggtatt tcgtgagaag ttcaacacca aaactggaac atagtctctcc ttcaagtgtt 60
 ggcgacagcg gggcttctctg attctggaat ataactttgt gtaaattaac agccacctat 120
 agaagagtcc atctgctgtg aaggagagac agagaactct gggttccgtc gtctctgtcca 180
 cgtgctgtac caagtgtgtg tgccagcctg ttacctgttc tcaactgaaa tctggctaatt 240
 gctcttgtgt atcacttctg attctgacaa tcaatcaatc aatggcctag agcactgact 300
 g 301

<210> 233
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 233
 atgactgact tcccagtaag gctctctaag gggtaagtag gaggatccac aggatttgag 60
 atgctaaggc cccagagatc gtttgatcca accctcttat ttccagaggg gaaaatgggg 120
 cctagaagtt acagagcatc tagctggtgc gctggcacc cttggcctcac acagactccc 180
 gagtagctgg gactacaggc acacagtcac tgaagcaggc cctgttagca attctatgcg 240
 tacaatttaa catgagatga gtagagactt tattgagaaa gcaagagaaa atcctatcaa 300
 c 301

<210> 234
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 234
 aggtcctaca catcgagact catccatgat tgatatgaat ttaaaaatta caagcaaaga 60
 cattttatc atcatgatgc tttcttttctg ttcttctttt cgttttcttc tttttctttt 120
 tcaatttcag caacatactt ctcaatttct tcaggattta aaatcttgag ggattgatct 180
 cgctcatga cagcaagtgc aatgtttttg ccacctgact gaaccacttc caggagtgcc 240
 ttgatcacca gcttaatggg cagatcatct gcttcaatgg cttcgtcagt atagttcttc 300
 t 301

<210> 235
 <211> 283
 <212> DNA
 <213> Homo sapien

<400> 235
 tggggctgtg catcaggcgg gtttgagaaa tattcaattc tcagcagaag ccagaatttg 60
 aattccctca tcttttaggg aatcatttac caggtttga gaggattcag acagctcagg 120
 tgctttcact aatgtctctg aacttctgtc cctctttgtt catggatagt ccaataaata 180
 atgttatctt tgaactgatg ctcataggag agaataaag aactctgagt gatatcaaca 240
 ttagggattc aaagaaatat tagatttaag ctcacactgg tca 283

<210> 236
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 236
 aggtcctcca ccaactgcct gaagcacggt taaaattggg aagaagtata gtgcagcata 60
 aatactttta aatcgatcag atttccctaa cccacatgca atcttcttca ccagaagagg 120
 tcggagcagc atcattaata ccaagcagaa tgcgtaatag ataaatacaa tggatatatg 180
 tgggtagacg gcttcatgag tacagtgtag tgtggtatcg taatctggac ttgggttgta 240
 aagcatcgtg taccagtcag aaagcatcaa tactcgacat gaacgaatat aaagaacacc 300
 a 301

<210> 237
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 237
 cagtggtagt ggtggtggac gtggcggttg tcgtggtgcc ttttttggtg cccgtcacaa 60
 actcaatttt tgttcegtcc tttttggcct ttcccaattt gtccatctca attttctggg 120
 ccttggtctaa tgcctcatag taggagtcct cagaccagcc atggggatca aacatatact 180
 ttgggtagtt ggtgccaaagc tcgtcaatgg cacagaatgg atcagcttct cgtaaatacta 240
 gggttccgaa attctttctt cctttggata atgtagtcca tatccattcc ctccctttatc 300
 t 301

<210> 238
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 238
 gggcagggttt tttttttttt ttttttgatg gtgcagaccc ttgctttatt tgtctgactt 60
 gttcacagtt cagccccctg ctccagaaaac caacgggcca gctaaggaga ggaggaggca 120
 ccttgagact tccggagtcg aggtctctca gggttcccca gcccatcaat cattttctgc 180
 accccctgcc tgggaagcag ctccctgggg ggtgggaatg ggtgactaga agggatttca 240
 gtgtgggacc cagggtctgt tcttcacagt aggaggtgga agggatgact aatttcttta 300
 t 301

<210> 239
 <211> 239
 <212> DNA
 <213> Homo sapien

<400> 239
 ataagcagct agggaattct ttatttagta atgtcctaac ataaaagtgc acataactgc 60
 ttctgtcaaa ccatgatact gagctttgtg acaaccaga aataactaag agaaggcaaa 120
 cataatacct tagagatcaa gaaacattta cacagtcaa ctgtttaaaa atagctcaac 180
 attcagccag tgagtagagt gtgaatgcc gcatcacag tatacagggtc cttcaggga 239

<210> 240

<211> 300
 <212> DNA
 <213> Homo sapien

<400> 240
 ggctcctaattg aagcagcagc ttccacatTT taacgcaggt ttacgggtgat actgtcctttt 60
 gggatctgcc ctccagtTga acctttttaag gaagaagtTg gcccaagcta agttccacat 120
 gctgggtgag ccagatgact tctgttccct ggTcactttc ttcaatgggg cgaatggggg 180
 ctgccaggtt tttaaaatca tgcttcatct tgaagcacac ggTcacttca ccctcctcac 240
 gctgtgggtg tactttgatg aaaataccca ctttTgtTggc ctttctgaag ctataatgtc 300

<210> 241
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 241
 gaggtctTgt gctgaggtct ctgggctagg aagaggagTt ctgtggagct ggaagccaga 60
 cctctttTga ggaaactcca gcagctatgt Tggtgtctct gagTgaatgc aacaaggctg 120
 ctctccatg tattggaaaa ctgcaaaactg gactcaactg gaaggaagtg ctgtTgccag 180
 Tgtgaagaac cagcctgagg tgacagaaac ggaagcaaac aggaacagcc agTcttttct 240
 tcctcctcct gTcatacggT ctctctcaag catcctTgt Tgtcaggggc ctaaaaggga 300
 g 301

<210> 242
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 242
 ccgaggTcct gggatgcaac caatcactct gttTcacgtg actttttatca ccatacaatt 60
 Tgtggcattt cctcattttc tacattgtag aatcaagagt gTaaataaat gtatatcgat 120
 gtcttcaaga atatatcatt cctttttcac tagaaccat tcaaaatata agTcaagaat 180
 cttaatatca acaaatatat caagcaaaact ggaaggcaga ataactacca taatttagta 240
 taagtaccca aagTttttata aatcaaaagc cctaattgata accattttta gaattcaatc 300
 a 301

<210> 243
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 243
 aggtaagtcc cagtttgaag ctcaaaagat ctggTatgag cataggctca Tcgacgacat 60
 ggtggcccaa gctatgaaat cagagggagg ctTcatctgT gcctgtaaaa actatgatTg 120
 TgacgtgCag Tcgactctg Tggcccaagg gtatggctct ctcggcata Tgaccagcgt 180
 gctggtttgt ccagatggca agacagtaga agcagaggct gccacggga ctgtTaaccg 240
 Tcactaccgc atgttccaga aaggacagga gacgtccacc aatccattg ctTccatttt 300
 t 301

<210> 244
 <211> 300
 <212> DNA
 <213> Homo sapien

<400> 244
 gctggtttgc aagaatgaaa TgaatgatTc tacagctagg acttaacctt gaaatggaaa 60
 gTcatgcaat ccattTgca ggaTctgtct gTgcacatgc ctctgtagag agcagcattc 120

ccagggacct	tgaaacagt	tgacactgta	aggtgcttgc	tccccaagac	acatectaaa	180
aggtgttgta	atggtgaaaa	cgtcttcctt	ctttattgcc	ccttcttatt	tatgtgaaca	240
actgtttgtc	ttttgtgtat	cttttttaaa	ctgtaaagtt	caattgtgaa	aatgaatatc	300

<210> 245

<211> 301

<212> DNA

<213> Homo sapien

<400> 245

gtctgagtat	ttaaaatggt	attgaaatta	tccccaacca	atgttagaaa	agaaagaggt	60
tatatactta	gataaaaaat	gaggtgaatt	actatccatt	gaaatcatgc	tcttagaatt	120
aaggccagga	gatattgtca	ttaatgtara	cttcaggaca	ctagagtata	gcagccctat	180
gttttcaaaag	agcagagatg	caattaaata	ttgttttagca	tcaaaaaggc	cactcaatac	240
agctaataaa	atgaaagacc	taatttctaa	agcaattcct	tataatttac	aaagttttaa	300
g						301

<210> 246

<211> 301

<212> DNA

<213> Homo sapien

<400> 246

ggtctgtcct	acaatgcctg	cttcttgaaa	gaagtcggca	ctttctagaa	tagctaaata	60
acctgggctt	attttaaaga	actatttgta	gctcagattg	gttttcctat	ggctaaaata	120
agtgccttct	gtgaaaatta	aataaaacag	ttaattcaaa	gccttgatat	atgttaccac	180
taacaatcat	actaaatata	ttttgaagta	caaagtttga	catgctctaa	agtgacaacc	240
caaatgtgtc	ttacaaaaca	cgcttcctaac	aaggtatgct	ttacactacc	aatgcagaaa	300
c						301

<210> 247

<211> 301

<212> DNA

<213> Homo sapien

<400> 247

aggtcctttg	gcagggctca	tggatcagag	ctcaaactgg	agggaaaggc	atttcgggta	60
gcctaagagg	gcgactggcg	gcagcacaac	caagggaaggc	aaggttgttt	ccccacgct	120
gtgtcctgtg	ttcaggtgcg	acacacaatc	ctcatgggaa	caggatcacc	catgcgctgc	180
ccttgatgat	caaggttggg	gcttaagtgg	attaaggag	gcaagttctg	ggttccttgc	240
cttttcaaac	catgaagtca	ggctctgtat	ccctcctttt	cctaactgat	attctaacta	300
a						301

<210> 248

<211> 301

<212> DNA

<213> Homo sapien

<400> 248

aggtccttgg	agatgccatt	tcagccgaag	gactcttctw	ttcggaagta	caccctcact	60
attaggaaga	ttcttagggg	taatttttct	gagggaaggag	aactagccaa	cttaagaatt	120
acaggaagaa	agtggtttgg	aagacagcca	aagaaataaa	agcagattaa	attgtatcag	180
gtacattcca	gcctgttggc	aactccataa	aaacatttca	gattttaatc	ccgaatttag	240
ctaattgagac	tggatttttg	ttttttatgt	tgtgtgtcgc	agagctaaaa	actcagttcc	300
c						301

<210> 249

<211> 301

<212> DNA

<213> Homo sapien

<400> 249

```

gtccagagga agcacctggg gctgaactag gcttgccctg ctgtgaactt gcacttggag      60
ccctgacgct gctgttctcc ccgaaaaacc cgaccgacct ccgcgatctc cgtcccgcgc      120
ccagggagac acagcagtgga ctcagagctg gtcgcacact gtgcctccct cctcaccgcc      180
catcgtaatg aattatcttg aaaattaatt ccaccatcct ttcagattct ggatggaaag      240
actgaatctt tgactcagaa ttgtttgctg aaaagaatga tgtgactttc ttagtcattt      300
a                                                                                   301

```

<210> 250

<211> 301

<212> DNA

<213> Homo sapien

<400> 250

```

ggtctgtgac aaggacttgc aggctgtggg aggcaagtga cccttaacac tacacttctc      60
cttatcttta ttggcttgat aaacataatt atttctaaca ctagcttatt tccagttgcc      120
cataagcaca tcagtacttt tctctggctg gaatagtaaa ctaaagtatg gtacatctac      180
ctaaaagact actatgtgga ataatacata ctaatgaagt attacatgat ttaaagacta      240
caataaaacc aaacatgctt ataacattaa gaaaaacaat aaagatacat gattgaaacc      300
a                                                                                   301

```

<210> 251

<211> 301

<212> DNA

<213> Homo sapien

<400> 251

```

gccgaggtcc tacatttggc ccagtttccc cctgcacact ctccaggggc cctgcctcat      60
agacaacctc atagagcata ggagaactgg ttgccctggg ggcaggggga ctgtctggat      120
ggcaggggtc ctcaaaaatg ccactgtcac tgccaggaaa tgcttctgag cagtacacct      180
cattggggtc aatgaaaagc ttcaagaaat cttcaggtcc actctcttga aggcccggaa      240
cctctggagg ggggcagtgg aatcccagct ccaggacgga tctgtctgaa aagatatcct      300
c                                                                                   301

```

<210> 252

<211> 301

<212> DNA

<213> Homo sapien

<400> 252

```

gcaaccaatc actctgtttc acgtgacttt tatcaccata caatttgtgg catttctctca      60
ttttctacat tgtagaatca agagtgtaaa taaatgtata tcgatgtctt caagaatata      120
tcattctctt ttcactagga acccattcaa aatataagtc aagaatctta atatcaacaa      180
atatatcaag caaactggaa ggcagaataa ctaccataat ttagtataag tacccaaagt      240
tttataaatc aaaagcccta atgataacca tttttagaat tcaatcatca ctgtagaatc      300
a                                                                                   301

```

<210> 253

<211> 301

<212> DNA

<213> Homo sapien

<400> 253

```

ttccctaaga agatgttatt ttgttgggtt ttgttcccc tccatctcga ttctcgtacc      60
caactaaaaa aaaaaaataa agaaaaaatg tgctgcgttc tgaaaaataa ctcttagct      120

```

```

tggtctgatt gttttcagac cttaaaatat aaacttgttt cacaagcttt aatccatgtg      180
gatttttttt cttagagaac cacaaaacat aaaaggagca agtcggactg aatacctgtt      240
tccatagtgc ccacagggtg ttcttcacat tttctccata ggaaaatgct ttttcccaag      300
g                                                                    301

```

```

<210> 254
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 254
cgctgcgctt ttcccttggg ggagggggcaa ggccagaggg ggtccaagtg cagcacgagg      60
aacttgacca attcccttga agcgggtggg ttaaaccctg taaatgggaa caaaatcccc      120
ccaaatctct tcatcttacc ctggtggact cctgactgta gaattttttg gttgaaacaa      180
gaaaaaaata aagcttttga cttttcaagg ttgcttaaca ggtactgaaa gactggcctc      240
acttaaaactg agccaggaaa agctgcagat ttattaatgg gtgtgttagt gtgcagtgcc      300
t                                                                    301

```

```

<210> 255
<211> 302
<212> DNA
<213> Homo sapien

```

```

<400> 255
agcttttttt tttttttttt tttttttttt ttcattaaaa aatagtgtct tttattataa      60
attactgaaa tgtttctttt ctgaatataa atataaatat gtgcaaagtt tgacttggat      120
tgggattttg ttgagttctt caagcatctc ctaataccct caagggcctg agtagggggg      180
agggaaaagg actggagggt gaatctttat aaaaaacaag agtgattgag gcagattgta      240
aacattatta aaaaacaaga aacaaacaaa aaaatagaga aaaaaaccac cccaacacac      300
aa                                                                    302

```

```

<210> 256
<211> 301
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

```

```

<400> 256
gttcagaaaa acattgaagg tggcttccca aagtctaaact agggataccc cctctagcct      60
aggaccctcc tccccacacc tcaatccacc aaaccatcca taatgcaccc agataggccc      120
acccccaaaa gcctggacac cttgagcaca cagttatgac caggacagac tcatctctat      180
aggcaaatag ctgctggcaa actggcatta cctggtttgt ggggatgggg gggcaagtgt      240
gtggcctctc ggctgggtta gcaagaacat tcagggtagg cctaagttan tcgtgttagt      300
t                                                                    301

```

```

<210> 257
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 257
gttggtggagg aactctggct tgctcattaa gtcctactga ttttactat ccctgaatt      60
tccccactta tttttgtctt tcaactatgc aggccttaga agaggtctac ctgcctccag      120
tcttacctag tccagtctac ccctggagt tagaatggcc atcctgaagt gaaaagtaat      180

```

```

gtcacattac tcccttcagt gattttctgt agaagtgcc atccctgaat gccaccaaga 240
tcttaatctt cacatcttta atcttatctc tttgactcct ctttacaccg gagaaggctc 300
c 301

```

```

<210> 258
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

```

```

<400> 258
cagcagtagt agatgccgta tgccagcacg cccagcactc ccaggatcag caccagcacc 60
aggggcccag ccaccaggcg cagaagcaag ataacacagta ggctcaagac cagagccacc 120
cccaggggcaa caagaatcca ataccaggac tgggcaaaaat cttcaaagat ctttaacactg 180
atgtctcggg cattgaggct gtcaataana cgctgatccc ctgctgtatg gtgggtgtcat 240
tgggtgatccc tgggagcgcc ggtggagtaa cgttggtcca tggaaagcag cgcccacaac 300
t 301

```

```

<210> 259
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

```

```

<400> 259
tcatatatgc aaacaaatgc agactangcc tcaggcagag actaaaggac atctcttggg 60
gtgtcctgaa gtgatttggg cccctgaggg cagacaccta agtaggaatc ccagtgggaa 120
gcaaagccat aaggaagccc aggattcctt gtgatcagga agtgggcccag gaaggctctgt 180
tccagctcac atctcatctg catgcagcac ggaccggatg cgcccactgg gtcttggcctt 240
ccctcccatc ttctcaagca gtgtccttgt tgagccattt gcaccttgg ctccagggtg 300
c 301

```

```

<210> 260
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 260
tttttttctt ccctaaggaa aaagaaggaa caagtctcat aaaaccaaat aagcaatggt 60
aagggtgtctt aacttgaaaa agattaggag tcaactggttt acaagttata attgaatgaa 120
agaactgtaa cagccacagt tggccatttc atgccaatgg cagcaaacia caggattaac 180
tagggcaaaa taaataagtg tgtggaagcc ctgataagt ctttaataaac agactgattc 240
actgagacat cagtacctgc ccgggcggcc gctcgagccg aattctgcag atatccatca 300
c 301

```

```

<210> 261
<211> 301
<212> DNA
<213> Homo sapien

```

<400> 261

aaatattcga gcaaatacctg taactaatgt gtctccataa aaggctttga actcagtga	60
tctgcttcca tccacgattc tagcaatgac ctctcggaca tcaaagctcc tcttaagggt	120
agcaccaact attccataca attcatcagc aggaaataaa ggctcttcag aagggttcaat	180
ggtgacatcc aattttcttct gataatttag attcctcaca accttcctag ttaagtgaag	240
ggcatgatga tcatccaaag cccagtggtc acttactcca gactttctgc aatgaagatc	300
a	301

<210> 262

<211> 301

<212> DNA

<213> Homo sapien

<400> 262

gaggagagcc tggtacagca tttgtaagca cagaatactc caggagtatt tgtaattgtc	60
tgtgagcttc ttgccgcaag tctctcagaa atttaaaaag atgcaaatcc ctgagtcacc	120
cctagacttc ctaaaccaga tctctcgggg ctggaacctg gcactctgca tttgtaatga	180
gggctttctg gtgcacacct aattttgtgc atctttgccc taaatcctgg attagtgcc	240
catcattacc cccacattat aatgggatag attcagagca gatactctcc agcaaagaat	300
c	301

<210> 263

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 263

tttagcttgt ggtaaatgac tcacaaaact gattttaaaa tcaagttaat gtgaattttg	60
aaaattacta cttaatccta attcacaata acaatggcat taaggtttga cttgagttgg	120
ttcttagtat tatattatgt aaataggctc ttaccacttg caaataactg gccacatcat	180
taatgactga ctccccagta aggtctctta aggggtaagt angaggatcc acaggatttg	240
agatgctaag gccccagaga tcgtttgatc caaccctctt attttcagag gggaaaatgg	300
g	301

<210> 264

<211> 301

<212> DNA

<213> Homo sapien

<400> 264

aaagacgtta aaccactcta ctaccacttg tggaactctc aaagggtaaa tgacaaascc	60
aatgaatgac tctaaaaaca atatttacat ttaatggttt gtagacaata aaaaaacaag	120
gtggatagat ctagaattgt aacattttta gaaaaccata scatttgaca gatgagaaag	180
ctcaattata gatgcaaagt tataactaaa ctactatagt agtaaagaaa tacatttcac	240
acccttcata taaattcact atcttggtt gaggcactcc ataaaatgta tcacgtgcat	300
a	301

<210> 265

<211> 301

<212> DNA

<213> Homo sapien

<400> 265

<210> 270
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 270
 cattgaagag cttttgcgaa acatcagaac acaagtgcctt ataaaattaa ttaagcctta 60
 cacaagaata catattcctt ttatttctaa ggagttaaac atagatgtag ctgatgtgga 120
 gagcttgctg gtgcagtga tattggataa cactattcat ggccgaattg atcaagtcaa 180
 ccaactcctt gaactggatc atcagaagaa ggggtggtgca cgatatactg cactagataa 240
 tggaccaacc aactaaattc tctcaccagg ctgtatcagt aaactggctt aacagaaaac 300
 a 301

<210> 271
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 271
 aaaagggttct cataagatta acaatttaaa taaatatttg atagaacatt ctttctcatt 60
 tttatagctc atcttttaggg ttgatattca gttcatgctt cccttgctgt tcttgatcca 120
 gaattgcaat cacttcatca gcctgtattc gctccaattc tctataaagt ggggtccaagg 180
 tgaaccacag agccacagca cacctctttc ccttggtgac tgccttcacc ccatganggt 240
 tctctcctcc agatganaac tgatcatgcg cccacatttt gggttttata gaagcagtca 300
 c 301

<210> 272
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 272
 taaattgcta agccacagat aacaccaatc aaatggaaca aatcactgtc ttcaaatgtc 60
 ttatcagaaa accaaatgag cctggaatct tcataatacc taaacatgcc gtatttagga 120
 tccaataatt ccctcatgat gagcaagaaa aattctttgc gcaccctcc tgcattccaca 180
 gcatcttctc caacaaatat aaccttgagt ggcttcttgt aatctatgtt ctttgttttc 240
 ctaaggactt ccattgcac tctacaata ttttctctac gcaccactag aattaagcag 300
 g 301

<210> 273
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 273
 acatgtgtgt atgtgtatct ttgggaaaan aanaagacat cttgtttayt atttttttgg 60
 agagangctg ggacatggat aatcacwtaa tttgctayta tyactttaat ctgactyga 120

```

gaaccgtcta aaaataaaat ttaccatgtc dtatatctct tatagtatgc ttatttcacc      180
ttytttctgt ccagagagag tatcagtgac ananatttma ggggtgaamac atgmattggg      240
gggacttnty tttacngagm accctgcccg sgcgcctctg makongantt ccgcsananc      300
t                                                                    301

```

```

<210> 274
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

```

```

<400> 274
cttatatact ctttctcaga ggcaaaagag gagatgggta atgtagacaa ttctttgagg      60
aacagtaaat gattattaga gagaangaat ggaccaagga gacagaaatt aacttgtaaa      120
tgattctctt tggaatctga atgagatcaa gaggccagct ttagcttggt gaaaagtcca      180
tctaggtatg gttgcattct cgtcttcttt tctgcagtag ataatgaggt aaccgaaggc      240
aattgtgctt cttttgataa gaagctttct tggtcatatc aggaaattcc aganaaagtc      300
c                                                                    301

```

```

<210> 275
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

```

```

<400> 275
tcggtgtcag cagcacgtgg cattgaacat tgcaatgtgg agcccaaacc acagaaaatg      60
gggtgaaatt ggccaacttt ctattaactt atgttggcaa ttttgccacc aacagtaagc      120
tggcccttct aataaaagaa aattgaaagg tttctcacta aacggaatta agtagtgagg      180
tcaagagact ccagggcctc agcgtacctg cccggggcggc cgctcgaagc cgaattctgc      240
agatatccat cacactggcg gncgctcgan catgcatcta gaaggnccaa ttcgccttat      300
a                                                                    301

```

```

<210> 276
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 276
tgtacacata ctcaataaat aaatgactgc attgtgggtat tattactata ctgattatat      60
ttatcatgtg acttctaatt agaaaatgta tccaaaagca aaacagcaga tatacaaaat      120
taaagagaca gaagatagac attaacagat aaggcaactt atacattgag aatccaaatc      180
caatacatth aaacatttgg gaaatgaggg ggacaaatgg aagccagatc aaatttgtgt      240
aaaactattc agtatgtttc ctttgcttca tgtctgagaa ggctctcctt caatggggat      300
g                                                                    301

```

```

<210> 277
<211> 301
<212> DNA
<213> Homo sapien

```

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 277
 tttgttgatg tcagtatttt attacttgcg ttatgagtgc tcacctggga aattctaaag 60
 atacagagga cttggaggaa gcagagcaac tgaatttaac ttaaaagaag gaaaacattg 120
 gaatcatggc actcctgata ctttcccaaa tcaacactct caatgcccc ccctcgtcct 180
 caccatagtg gggagactaa agtggccacg gatttgccctt angtgtgcag tgcgttctga 240
 gttcncgtgc gattacatct gaccagtctc ctttttccga agtccttccg ttcaatcttg 300
 c 301

<210> 278
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 278
 taccactaca ctccagcctg ggcaacagag caagacctgt ctcaaagcat aaaatggaat 60
 aacatatcaa atgaaacagg gaaaatgaag ctgacaattt atggaagcca gggcttgtca 120
 cagtctctac tgttattatg cattacctgg gaatttatat aagcccttaa taataatgcc 180
 aatgaacatc tcatgtgtgc tcacaatggt ctggcactat tataagtgtc tcacaggttt 240
 tatgtgttct tcgtaacttt atggantagg tactcggccg cgaacacgct aagccgaatt 300
 c 301

<210> 279
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 279
 aaagcaggaa tgacaaagct tgcttttctg gtatgttcta ggtgtattgt gacttttact 60
 gttatatata ttgccaatat aagtaaatat agattatata tgtatagtgt ttcacaaagc 120
 ttagaccttt accttcacag caccacacag tgcttgatat ttcagagtca gtcattgggt 180
 atacatgtgt agttccaaag cacataagct agaanaanaa atatttctag ggagcactac 240
 catctgtttt cacatgaaat gccacacaca tagaactcca acatcaattt cattgcacag 300
 a 301

<210> 280
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 280
 ggtactggag ttttctctcc ctgtgaaaac gtaactactg ttgggagtga attgaggatg 60
 tagaaagggt gtggaaccaa attgtggtca atggaaatag gagaatatgg ttctcactct 120

tgagaaaaaa	acctaagatt	agcccaggta	gttgccctgta	acttcagttt	ttctgcctgg	180
gtttgatata	gttttagggt	ggggtagat	taagatctaa	attacatcag	gacaaagaga	240
cagactatta	actccacagt	taattaagga	ggtatgttcc	atgtttattt	gttaaagcag	300
t						301

<210> 281
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 281						
aggtacaaga	aggggaatgg	gaaagagctg	ctgctgtggc	attgttcaac	ttggatattc	60
gccgagcaat	ccaaatcctg	aatgaagggg	catcttctga	aaaaggagat	ctgaatctca	120
atgtggtagc	aatggcttta	tcgggttata	cggatgagaa	gaactccctt	tgagagagaa	180
tgtgtagcac	actgcgatta	cagctaaata	acccgtattt	gtgtgtcatg	tttgcatttc	240
tgacaagtga	aacaggatct	tacgatggag	ttttgtatga	aaacaaagtt	gcagtacctc	300
g						301

<210> 282
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 282						
cagggtactac	agaattaaaa	tactgacaag	caagtagttt	cttggcgtgc	acgaattgca	60
tccagaaccc	aaaaattaa	aaattcaaaa	agacattttg	tgggcacctg	ctagcacaga	120
agcgcagaag	caaagcccag	gcagaacat	gctaaccctt	cagctcagcc	tgacacagaag	180
cgcagaagca	aagcccaggc	agaaccatgc	taaccttaca	gctcagcctg	cacagaagcg	240
cagaagcaaa	gcccaggcag	aacatgctaa	ccttacagct	cagcctgca	agaagcacag	300
a						301

<210> 283
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 283						
atctgtatac	ggcagacaaa	ctttatarag	tgtagagagg	tgagcgaaag	gatgcaaaag	60
cactttgagg	gctttataat	aatatgctgc	ttgaaaaaaa	aaatgtgtag	ttgatactca	120
gtgcatctcc	agacatagta	aggggttgct	ctgaccaatc	aggatgatcat	tttttctatc	180
acttcccagg	ttttatgcaa	aaattttgtt	aaattctata	atgggtgatat	gcatctttta	240
ggaaacatat	acatttttaa	aatcttattt	tatgtaagaa	ctgacagacg	aatttgcttt	300
g						301

<210> 284
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 284						
cagggtacaaa	acgctattaa	gtggcttaga	atttgaacat	ttgtggctctt	tatttacttt	60
gcttcgtgtg	tgggcaaagc	aacatcttcc	ctaaatatat	attaccaaga	aaagcaagaa	120
gcagattagg	tttttgacaa	aacaacacag	ccaaaagggg	gctgacctgg	agcagagcat	180
ggtagagagg	aaggcatgag	agggcaagtt	tgttgtggac	agatctgtgc	ctactttatt	240
actggagtaa	aagaaaacaa	agttcattga	tgtcgaagga	tatatacagt	gttagaaatt	300
a						301

<210> 285

<211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 285
 acatcaccat gatcggtacc cccacccatt atacgttgta tgtttacata aatactcttc 60
 aatgatcatt agtgttttaa aaaaaatact gaaaactcct tctgcatccc aatctctaac 120
 caggaaagca aatgctatct acagacctgc aagccctccc tcaaacnaaa ctatttctgg 180
 attaaatag tctgacttct tttgaggcca cagcactagg caaatgctat ttacgatctg 240
 caaaagctgt ttgaagagtc aaagcccca tgtgaacacg atttctggac cctgtaacag 300
 t 301

<210> 286
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 286
 taccactgca ttccagcctg ggtgacagag tgagactccg tctccaaaaa aaactttgct 60
 tgtatattat ttttgcccta cagtggatca ttctagtagg aaaggacagt aagatttttt 120
 atcaaaatgt gtcattgccag taagagatgt tatattcttt tctcatttct tccccacca 180
 aaaataagct accatatagc ttataagtct caaatttttg ccttttacta aaatgtgatt 240
 gtttctgttc attgtgtatg cttcatcacc tatattaggc aaattccatt tttcccttg 300
 t 301

<210> 287
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 287
 tacagatctg ggaactaaat attaaaaatg agtgtggctg gatatatgga gaatgttggg 60
 cccagaagga acgtagagat cagatattac aacagctttg ttttgagggt tagaaatag 120
 aaatgatttg gttatgaacg cacagttagg gcagcagggc cagaatcctg accctctgcc 180
 ccgtggttat ctctcccca gcttggtcgc ctcagtgtat cacagtattc cattttgttt 240
 gttgcatgtc ttgtgaagcc atcaagattt tctcgtctgt tttcctctca ttggaatgc 300
 t 301

<210> 288
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 288
 gtacacctaa ctgcaaggac agctgaggaa tgtaatgggc agccgctttt aaagaagtag 60
 agtcaatagg aagacaaatt ccagttccag ctcagtctgg gtatctgcaa agctgcaaaa 120
 gatcttttaa gacaatttca agagaatatt tccttaaagt tggcaatttg gagatcatac 180
 aaaagcatct gcttttgtga tttaatttag ctcactctgg cactggaaga atccaaacag 240
 tctgccttaa ttttggtatg atgcatgatg gaaattcaat aatttagaaa gttaaaaaaa 300
 a 301

<210> 289
 <211> 301

<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 289
ggtacactgt ttccatgtta tgtttctaca cattgctacc tcagtgtccc tggaaactta 60
gcttttgatg tctccaagta gtccaccttc atttaactct ttgaaactgt atcatccttg 120
ccaagtaaga gtggtggcct atttcagctg ctttgacaaa atgactggct cctgacttaa 180
cgttctataa atgaatgtgc tgaagcaaag tgcccatggg ggcggcgaan aagagaaaaga 240
tgtgttttgt tttggactct ctgtgggtccc ttccaatgct gtgggtttcc aaccagngga 300
a 301

<210> 290
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 290
acactgagct cttcttgata aatatacaga atgcttggca tatacaagat tctatactac 60
tgactgatct gttcatttct ctcacagctc ttaccccca aagcttttcc accctaagtg 120
ttctgacctc cttttctaat cacagtaggg atagaggcag anccacctac aatgaacatg 180
gagttctatc aagaggcaga aacagcacag aatcccagtt ttaccattcg ctagcagtgc 240
tgccttgaac aaaaacattt ctccatgtct cattttcttc atgcctcaag taacagtgag 300
a 301

<210> 291
<211> 301
<212> DNA
<213> Homo sapien

<400> 291
caggtaacca tttcttctat cctagaaaca tttcatttta tgttggtgaa acataacaac 60
tatatcagct agattttttt tctatgcttt acctgctatg gaaaatttga cacattctgc 120
tttactcttt tgtttatagg tgaatcacia aatgtatttt tatgtattct gtagtccaat 180
agccatggct gtttacttca tttaatttat ttagcataaa gacattatga aaaggcctaa 240
acatgagctt cacttcccca ctaactaatt agcatctggt atttcttaac cgtaatgcct 300
a 301

<210> 292
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 292

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accttttagt agtaatgtct aataataaat aagaaatcaa ttttataagg tccatatagc      60
tgtattaaat aatttttaag tttaaaagat aaaataccat catttttaaat gttggtattc      120
aaaaccaaag natataaccg aaaggaaaaa cagatgagac ataaaatgat ttgcnagatg      180
ggaaatatag tasttyatga atgttnatta aattccagtt ataatagtgg ctacacactc      240
tcactacaca cacagacccc acagtcctat atgccacaaa cacatttcca taacttgaaa      300
a                                                                                   301

```

<210> 293

<211> 301

<212> DNA

<213> Homo sapien

<400> 293

```

ggtaccaagt gctggtgcca gcctgttacc tgttctcact gaaaagtctg gctaattgctc      60
ttgtgtagtc acttctgatt ctgacaatca atcaatcaat ggcctagagc actgactgtt      120
aacacaaaacg tcactagcaa agtagcaaca gctttaagtc taaatacaaa gctgttctgt      180
gtgagaattt tttaaaaggc tacttgtata ataacccttg tcatttttaa tgtacctcgg      240
ccgcgaccac gctaagccga attctgcaga tatecatcac actggcggcc gctcgagcat      300
g                                                                                   301

```

<210> 294

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 294

```

tgaccataa caatatacac tagctatctt tttactgtc catcattagc accaatgaag      60
attcaataaa attaccttta ttcacacatc tcaaaacaat tctgcaaatt cttagtgaag      120
tttaactata gtcacaganc ttaaattatc acattgtttt ctatgtctac tgaaaataag      180
ttcactactt ttctgggata ttctttacaa aatcttatta aaattcctgg tattatcacc      240
cccaattata cagtagcaca accaccttat gtagttttta catgatagct ctgtagaggt      300
t                                                                                   301

```

<210> 295

<211> 305

<212> DNA

<213> Homo sapien

<400> 295

```

gtactctttc tctccctccc tctgaattta attctttcaa cttgcaattt gcaaggatta      60
cacatttcac tgtgatgtat attgtgttgc aaaaaaaaaa gtgtctttgt ttaaaattac      120
ttgggtttgtg aatccatctt gctttttccc cattggaact agtcattaac ccatctctga      180
actggtagaa aaacrtctga agagctagtc tatcagcatc tgacagggtga attggatggg      240
tctcagaacc atttcaccca gacagcctgt ttctatcctg ttttaataaat tagtttgggt      300
tctct                                                                                   305

```

<210> 296

<211> 301

<212> DNA

<213> Homo sapien

<400> 296

```

aggtagctat ggaagctgct aaaataatat ttgatagtaa aagtagtaa tgtgctatct      60

```



```

cacctagtag taaactaaaa ataaactgaa actttatgga atctgaagtt attttccttg      120
attaatataga attaataaac caatatgagg aaacatgaaa ccatgcaatc tactatcaac      180
tttgaaaaag tgattgaacg aaccacttag ctttcagatg atgaacactg ataagtcatt      240
tgtcattact ataaatttta aaatctgtta ataagatggc ctatagggag gaaaaagggg      300
c                                                                                   301

```

```

<210> 297
<211> 300
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(300)
<223> n = A,T,C or G

```

```

<400> 297
actgagtttt aactggacgc caagcaggca aggctggaag gttttgctct ctttgtgcta      60
aaggttttga aaaccttgaa ggagaatcat tttgacaaga agtacttaag agtctagaga      120
acaaagangt gaaccagctg aaagctctcg ggggaanctt acatgtgttg ttaggcctgt      180
tccatcattg ggagtgcaact ggccatccct caaaatttgt ctgggctggc ctgagtggtc      240
accgcacctc ggccgcgacc acgctaagcc gaattctgca gatatccatc aactggcgg      300

```

```

<210> 298
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

```

```

<400> 298
tatggggttt gtcacccaaa agctgatgct gagaaaggcc tccctggggc cctccccgcg      60
ggcatctgag agacctggtg ttccagtgtt tctggaaatg ggtcccagtg ccgccggctg      120
tgaagctctc agatcaatca cgggaagggc ctggcgggtg tggccacctg gaaccacct      180
gtcctgtctg tttacatttc actaycaggt tttctctggg cattacnatt tgttccccta      240
caacagtgac ctgtgcattc tgctgtggcc tgctgtgtct gcagggtggt ctcagcgagg      300
t                                                                                   301

```

```

<210> 299
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 299
gttttgagac ggagtttcac tcttgttgcc cagactggac tgcaatggca gggctctctgc      60
tcactgcacc ctctgcctcc caggttcgag caattctcct gcctcagcct cccaggtagc      120
tgggattgca ggctcacgcc accataccca gctaattttt ttgtattttt agtagagacg      180
gagtttcgcc atggtggcca gctgggtctca aactcctgac ctcaagcgac ctgcctgcct      240
cggcctccca aagtgtctga attataggca tgagtcaaca cgcccagcct aaagatattt      300
t                                                                                   301

```

```

<210> 300
<211> 301
<212> DNA
<213> Homo sapien

```

<400> 300
 attcagtttt atttgetgcc ccagtatctg taaccaggag tgccacaaaa tcttgccaga 60
 tatgtccac acccactggg aaaggctccc acctggctac ttctctatc agctgggtca 120
 gctgcattcc acaaggttct cagcctaag agtttacta cctgccagtc tcaaaactta 180
 gtaaaagcaag accatgacat tccccacgg aaatcagagt ttgccccacc gtcttggtac 240
 tataaagcct gcctctaaca gtccttgctt cttcacacca atcccgagcg catcccccat 300
 g 301

<210> 301
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 301
 tttaaattttt gagaggataa aaaggacaaa taatctagaa atgtgtcttc ttcagtctgc 60
 agaggacccc aggtctccaa gcaaccacat ggtcaagggc atgaataatt aaaagtgtgt 120
 gggaaactcac aaagaccctc agagctgaga caccacaaac agtgggagct cacaagacc 180
 ctgagagctg agacacccac aacagtggga gtcacaaaag accctcagag ctgagacacc 240
 cacaacagca cctcgttcag ctgccacatg tgtgaataag gatgcaatgt ccagaagtgt 300
 t 301

<210> 302
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 302
 aggtacacat ttagcttgtg gtaaatgact cacaaaactg attttaaaat caagttaatg 60
 tgaattttga aaattactac ttaatcctaa ttcacaataa caatggcatt aaggtttgac 120
 ttgagttggt tcttagtatt atttatggta aataggctct taccacttgc aaataactgg 180
 ccacatcatt aatgactgac ttcccagtaa ggctctctaa ggggtaagta ggaggatcca 240
 caggatttga gatgctaagg ccccagagat cgtttgatcc aaccctctta ttttcagagg 300
 g 301

<210> 303
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 303
 aggtaccaac tgtggaaata ggtagaggat cattttttct ttccatatca actaagttgt 60
 atattgtttt ttgacagttt aacacatctt cttctgtcag agattcttcc acaatagcac 120
 tggctaattg aactaccgct tgcattgtaa aaatgggtgt ttgtgaaatg atcataggcc 180
 agtaacgggt atgtttttct aactgatctt ttgctcgttc caaagggacc tcaagacttc 240
 catcgatttt atatctgggg tctagaaaag gagttaatct gttttccctc ataaattcac 300
 c 301

<210> 304
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 304
 acatggatgt tattttgcag actgtcaacc tgaatttgta tttgcttgac attgcctaatt 60
 tattagtttc agtttcagct taccactttt ttgtctgcaa catgcaraas agacagtgcc 120
 ctttttagtg tatcatatca ggaatcatct cacattgggt tgtgccatta ctggtgcagt 180
 gactttcagc cacttgggta aggtggagtt ggccatatgt ctccactgca aaattactga 240

ttttcctttt gtaattaata agtgtgtgtg tgaagattct ttgagatgag gtatatatct 300
c 301

<210> 305

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 305

gangtacagc	gtggtcaagg	taacaagaag	aaaaaatgt	gagtggcatc	ctgggatgag	60
cagggggaca	gacctggaca	gacacgttgt	catttgctgc	tgtgggtagg	aaaatgggcg	120
taaaggagga	gaaacagata	caaatctcc	aactcagtat	taaggatttc	tcatgcctag	180
aatattggta	gaaacaagaa	tacattcata	tggcaataa	ctaaccatgg	tggacaacaaa	240
ttctgggatt	taagttggat	accaangaaa	ttgtattaaa	agagctgttc	atggaataag	300
a						301

<210> 306

<211> 8

<212> PRT

<213> Homo sapien

<400> 306

Val	Leu	Gly	Trp	Val	Ala	Glu	Leu
1				5			

<210> 307

<211> 637

<212> DNA

<213> Homo sapien

<400> 307

acagggratg	aagggaagg	gagaggatga	ggaagcccc	ctggggattt	ggtttgggtcc	60
ttgtgatcag	gtggtctatg	gggcttatcc	ctacaaagaa	gaatccagaa	ataggggcac	120
attgaggaat	gatacttgag	cccaaagagc	attcaatcat	tgttttattt	gccttmtttt	180
cacaccattg	gtgagggagg	gattaccacc	ctggggttat	gaagatgggt	gaacacccca	240
cacatagcac	cggagatatg	agatcaacag	tttcttagcc	atagagattc	acagcccaga	300
gcaggaggac	gcttgccacac	catgcaggat	gacatggggg	atgcgctcgg	gattgggtgtg	360
aagaagcaag	gactgttaga	ggcaggcttt	atagtaacaa	gacgggtggg	caaactctga	420
tttccgtggg	ggaatgtcat	ggtcttgctt	tactaagttt	tgagactggc	aggtagtgaa	480
actcattagg	ctgagaacct	tgtggaatgc	acttgacca	sctgatagag	gaagtagcca	540
ggtgggagcc	tttcccagtg	ggtgtgggac	atatctggca	agattttgtg	gcactcctgg	600
ttacagatac	tggggcagca	aataaaactg	aatcttg			637

<210> 308

<211> 647

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(647)

<223> n = A,T,C or G

<400> 308

acgattttca	ttatcatgta	aatcgggtca	ctcaaggggc	caaccacagc	tgggagccac	60
tgctcagggg	aaggttcata	tgggactttc	tactgcccaa	ggttctatac	aggatataaa	120
ggngcctcac	agtatagatc	tggtagcaaa	gaagaagaaa	caaacactga	tctctttctg	180
ccaccctct	gaccctttgg	aactcctctg	accctttaga	acaagcctac	ctaatatctg	240
ctagagaaaa	gaccaacaac	ggcctcaaag	gatctcttac	catgaaggtc	tcagctaatt	300
cttggctaag	atgtgggttc	cacattaggt	tctgaatatg	gggggaaggg	tcaatttgct	360
catttttgtt	gtggataaag	tcaggatgcc	caggggccag	agcagggggc	tgcttgcttt	420
gggaacaatg	gctgagcata	taaccatagg	ttatggggaa	caaaacaaca	tcaaagtcac	480
tgtatcaatt	gccatgaaga	cttgagggac	ctgaatctac	cgattcatct	taaggcagca	540
ggaccagttt	gagtggcaac	aatgcagcag	cagaatcaat	ggaaacaaca	gaatgattgc	600
aatgtccttt	ttttctcct	gcttctgact	tgataaaaag	ggaccgt		647

<210> 309

<211> 460

<212> DNA

<213> Homo sapien

<400> 309

actttatagt	ttaggctgga	cattggaaaa	aaaaaaaagc	cagaacaaca	tgtgatagat	60
aatatgattg	gctgcacact	tccagactga	tgaatgatga	acgtgatgga	ctattgtatg	120
gagcacatct	tcagcaagag	ggggaaatac	tcatcatttt	tggccagcag	ttgtttgatc	180
accaaacatc	atgccagaat	actcagcaaa	ccttcttagc	tcttgagaag	tcaaagtcag	240
gggggaattt	ttcctggcaa	ttttaattgg	actccttatg	tgagagcagc	ggctaccag	300
ctgggggtgt	ggagcgaacc	cgtcactagt	ggacatgcag	tggcagagct	cctggtaacc	360
acctagagga	atacacaggc	acatgtgtga	tgccaagcgt	gacacctgta	gcaactcaat	420
ttgtcttgtt	tttgtctttc	ggtgtgtaag	attcttaagt			460

<210> 310

<211> 539

<212> DNA

<213> Homo sapien

<400> 310

acgggactta	tcaataaaag	ataggaaaag	aagaaaactc	aaatattata	ggcagaaatg	60
ctaaagggtt	taaaatatgt	caggattgga	agaaggcatg	gataaagaac	aaagttcagt	120
taggaaaagag	aaacacagaa	ggaagagaca	caataaaaag	cattatgtat	tctgtgagaa	180
gtcagacagt	aagatttgtg	ggaaatgggt	tggtttgttg	tatggtatgt	attttagcaa	240
taatctttat	ggcagagaaa	gctaaaatcc	tttagcttgc	gtgaatgatc	acttgctgaa	300
ttcctcaagg	taggcatgat	gaaggagggt	ttagaggaga	cacagacaca	atgaactgac	360
ctagatagaa	agccttagta	tactcagcta	ggaatagtga	ttctgagggc	acactgtgac	420
atgattatgt	cattacatgt	atggtagtga	tggggatgat	aggaagggaag	aacttatggc	480
atattttcac	ccccacaaaa	gtcagttaaa	tattggggaca	ctaaccatcc	aggtaaga	539

<210> 311

<211> 526

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)... (526)

<223> n = A,T,C or G

<400> 311

caaatttgag	ccaatgacat	agaattttac	aatcaagaa	gcttattctg	gggccatttc	60
ttttgacgtt	ttctctaaac	tactaaagag	gcattaatga	tccataaatt	atattatcta	120
catttacagc	atttaaaatg	tgttcagcat	gaaatattag	ctacagggga	agctaaataa	180

attaacatg	gaataaagat	ttgtccttaa	atataatcta	caagaagact	ttgatatttg	240
tttttcacaa	gtgaagcatt	cttataaagt	gtcataacct	ttttggggaa	actatgggaa	300
aaaatgggga	aactctgaag	ggttttaagt	atcttacctg	aagctacaga	ctccataacc	360
tctctttaca	gggagctcct	gcagccccta	cagaaatgag	tggctgagat	tcttgattgc	420
acagcaagag	cttctcatct	aaaccctttc	cctttttagt	atctgtgtat	caagtataaa	480
agttctataa	actgtagtnt	acttatttta	atccccaag	cacagt		526

<210> 312

<211> 500

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)... (500)

<223> n = A,T,C or G

<400> 312

cctctctctc	cccacccct	gactctagag	aactggggtt	tctcccagta	ctccagcaat	60
tcattttctga	aagcagttga	gccactttat	tccaaagtac	actgcagatg	ttcaaactct	120
ccattttctc	ttcccttcca	cctgccagtt	ttgctgactc	tcaacttgtc	atgagtgtaa	180
gcatttaagga	cattatgctt	cttcgattct	gaagacaggc	cctgctcatg	gatgactctg	240
gcttcttagg	aaaatatttt	tcttccaaaa	tcagtaggaa	atctaaactt	atccccctct	300
tgcagatgtc	tagcagcttc	agacatttgg	ttaagaacct	atgggaaaaa	aaaaaatcct	360
tgctaattgt	gtttcctttg	ttaaccanga	ttcttatttg	nctggtatag	aatatcagct	420
ctgaacgtgt	ggtaaagatt	tttgtgtttg	aatataggag	aatcagttt	gctgaaaagt	480
tagtcttaat	tatctattgg					500

<210> 313

<211> 718

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)... (718)

<223> n = A,T,C or G

<400> 313

ggagatttgt	gtggtttgca	gccgaggag	accaggaaga	tctgcatggt	gggaaggacc	60
tgatgataca	gaggtgagaa	ataagaaagg	ctgctgactt	taccatctga	ggccacacat	120
ctgctgaaat	ggagataatt	aacatcacta	gaaacagcaa	gatgacaata	taatgtctaa	180
gtagtgacat	gtttttgcac	atttccagcc	cttttaaata	tccacacaca	caggaagcac	240
aaaagggaagc	acagagatcc	ctgggagaaa	tgcccggccg	ccatcttggg	tcacgatga	300
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cgttatacca	atcatttcta	tttctaccct	caaacaagct	gtngaataatc	tgacttacgg	660
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<210> 314

<211> 358

<212> DNA

<213> Homo sapien

<400> 314

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caacatgtgt	agatctcttg	tcttattctt	ttgtctataa	tactgtattg	tgtagtccaa	180
gctctcggtg	gtccagccac	tgtgaaacat	gctcccttta	gattaacctc	gtggacgctc	240
ttgttgatt	gctgaactgt	agtgcctgt	attttgcttc	tgtctgtgaa	ttctgttgct	300
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<210> 315

<211> 341

<212> DNA

<213> Homo sapien

<400> 315

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gacccccatt	ctgaagatgt	ctggaacctc	taccagcagg	atgatgatag	ccccaatgac	180
agtcaccagc	tccccgacca	gccggatata	gtccttaggg	gtcatgtagg	cttctgaag	240
tagcttctgc	tgtaagagg	tggtgtcccg	ggggctcgtg	cggttattgg	tctgggctt	300
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<210> 316

<211> 151

<212> DNA

<213> Homo sapien

<400> 316

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cattcaggga	gctctggttg	caatattagt	t			151

<210> 317

<211> 151

<212> DNA

<213> Homo sapien

<400> 317

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atcttcattt	atctctggcc	ttaacctgg	ctcctgaggc	tgcgccagc	agatcccagg	120
ccagggtct	gttcttgcca	cacctgcttg	a			151

<210> 318

<211> 151

<212> DNA

<213> Homo sapien

<400> 318

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<210> 319

<211> 151

<212> DNA

<213> Homo sapien

<400> 319

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taagattggg tttatgtgat tttagtgggt a 151

<210> 320
<211> 150
<212> DNA
<213> Homo sapien

<400> 320
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gagcggctgc cctttttttt tttttttttg ggggggaatt tttttttttt aatagttatt 120
gagtgttcta cagcttacag taaataccat 150

<210> 321
<211> 151
<212> DNA
<213> Homo sapien

<400> 321
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tgctctgag aaatcaaagt cttcatacac t 151

<210> 322
<211> 151
<212> DNA
<213> Homo sapien

<220>
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<222> (1)...(151)
<223> n = A,T,C or G

<400> 322
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attgtgcagg gctcgttcca nacttccagt t 151

<210> 323
<211> 151
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(151)
<223> n = A,T,C or G

<400> 323
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nagactcant tactaccag tttgtggtt twtgggagaa atgtaactgg acagttagct 120
gttcaatyaa aaagacactt ancccatgtg g 151

<210> 324
<211> 461
<212> DNA
<213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(461)
 <223> n = A,T,C or G

<400> 324
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 agaagtgggtc agctaaagga atccagggtt ttgggttgac tgtaataacc tttgatgaaa 120
 agagttacta cgaatcccat cttgggttcca gctatatcac tgacagcatg gtagaagact 180
 gcgaacctca cttctagact ttcacgggtg gacgaaacgg gttcagaaac tgccaggggc 240
 ctcatcacagg gatatacaaaa taccctttgt gctacccagg ccctggggaa tcagggtgact 300
 cacacaaatg caatagttgg tcaactgcatt tttacctgaa ccaaagctaa acccggtgtt 360
 gccaccatgc accatggcat gccagagttc aacactgttg ctcttgaaaa ttgggtctga 420
 aaaaacgcac aagagccct gccctgcct agctgangca c 461

<210> 325
 <211> 400
 <212> DNA
 <213> Homo sapien

<400> 325
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<210> 326
 <211> 1215
 <212> DNA
 <213> Homo sapien

<400> 326
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 aaaaaaaaaa aaaaa 1215

<210> 327
 <211> 220

<212> PRT

<213> Homo sapien

<400> 327

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Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp	Val
			20				25					30			
Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu	Gly
		35					40					45			
Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val	Glu
	50					55					60				
Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro	Leu	Leu	Ala
65				70						75				80	
Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser	Glu	Ser	Asp
			85					90					95		
Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr	Ala	Gly	Asn
			100					105					110		
Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Gly	Arg	Met	Pro
		115					120					125			
Thr	Val	Leu	Gln	Cys	Val	Asn	Val	Ser	Val	Val	Ser	Glu	Glu	Val	Cys
	130					135					140				
Ser	Lys	Leu	Tyr	Asp	Pro	Leu	Tyr	His	Pro	Ser	Met	Phe	Cys	Ala	Gly
145				150						155				160	
Gly	Gly	Gln	Asp	Gln	Lys	Asp	Ser	Cys	Asn	Gly	Asp	Ser	Gly	Gly	Pro
			165						170				175		
Leu	Ile	Cys	Asn	Gly	Tyr	Leu	Gln	Gly	Leu	Val	Ser	Phe	Gly	Lys	Ala
			180					185					190		
Pro	Cys	Gly	Gln	Val	Gly	Val	Pro	Gly	Val	Tyr	Thr	Asn	Leu	Cys	Lys
		195					200					205			
Phe	Thr	Glu	Trp	Ile	Glu	Lys	Thr	Val	Gln	Ala	Ser				
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<210> 328

<211> 234

<212> DNA

<213> Homo sapien

<400> 328

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atccgcagtg	ggtgctgtca	gccacacact	gtttccagaa	ctcctacacc	atcgggctgg	180
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<210> 329

<211> 77

<212> PRT

<213> Homo sapien

<400> 329

Leu	Val	Ser	Gly	Ser	Cys	Ser	Gln	Ile	Ile	Asn	Gly	Glu	Asp	Cys	Ser
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Pro	His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Val	Met	Glu	Asn	Glu	Leu
			20				25					30			
Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp	Val	Leu	Ser	Ala	Thr
		35					40					45			
His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu	Gly	Leu	His	Ser	Leu
	50					55					60				

Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu Ala
 65 70 75

<210> 330
 <211> 70
 <212> DNA
 <213> Homo sapien

<400> 330
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 gctgcagcca 70

<210> 331
 <211> 22
 <212> PRT
 <213> Homo sapien

<400> 331
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 1 5 10 15
 Val Ser Gly Ser Cys Ser
 20

<210> 332
 <211> 2507
 <212> DNA
 <213> Homo sapien

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<210> 333

<211> 3030

<212> DNA

<213> Homo sapien

<400> 333

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<210> 334

<211> 2417

<212> DNA

<213> Homo sapien

<400> 334

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<211> 2984

<212> DNA

<213> Homo sapien

<400> 335

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 <212> PRT
 <213> Homo sapien

<400> 336
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 35 40 45
 Val Ile Glu Leu Glu Arg Lys Phe Ser His Gln Lys Tyr Leu Ser Ala
 50 55 60
 Pro Glu Arg Ala His Leu Ala Lys Asn Leu Lys Leu Thr Glu Thr Gln
 65 70 75 80
 Val Lys Ile Trp Phe Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln
 85 90 95
 Leu Ser Ser Glu Leu Gly Asp Leu Glu Lys His Ser Ser Leu Pro Ala
 100 105 110
 Leu Lys Glu Glu Ala Phe Ser Arg Ala Ser Leu Val Ser Val Tyr Asn
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 Ser Tyr Pro Tyr Tyr Pro Tyr Leu Tyr Cys Val Gly Ser Trp Ser Pro
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 Ala Phe Trp
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<210> 337
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 <212> PRT
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<400> 337
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<210> 338
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<210> 339
 <211> 318
 <212> PRT
 <213> Homo sapien

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Val	Ala	Lys	Glu	Ile	Gln	Thr	Thr	Thr	Gly	Asn	Gln	Gln	Val	Leu	Val
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Ser	Leu	Ala	His	His	Leu	Gly	Arg	Ile	His	Phe	His	Asn	Leu	Gln	Gly
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Glu	Lys	Phe	Tyr	Asn	Ala	Gly	Leu	Ala	Tyr	Cys	His	Ser	Lys	Leu	Ala
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			245						250					255	
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			260					265					270		
Thr	Glu	Gly	Leu	Glu	Ile	Leu	Ser	Gly	Asn	His	Phe	Ser	Asp	Cys	His
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Val	Ala	Trp	Val	Ser	Ala	Gln	Ala	Arg	Asn	Glu	Thr	Ile	Ala	Arg	Arg
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<210> 340

<211> 483

<212> DNA

<213> Homo sapien

<400> 340

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gctccaaacg	tgacatcact	gatgctcttc	tcggggggtgc	tgatggcccg	cttgggtcacg	360
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<210> 341

<211> 344

<212> DNA

<213> Homo sapien

<400> 341

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gctgccttac	aagtattaaa	tattttactt	ctttccataa	agagtagctc	aaaatatgca	180
attaatttaa	taattttctga	tgatggtttt	atctgcagta	atatgtatat	catctattag	240
aattttactta	atgaaaaact	gaagagaaca	aaatttgtaa	ccactagcac	ttaagtactc	300
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<210> 342

<211> 592

<212> DNA

<213> Homo sapien

<400> 342

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caatgtggaa	acttcttata	cttggttcca	ttatgaagtt	ggacaattgc	tgctatcaca	120
cctggcaggt	aaaccaatgc	caagagagtg	atggaaacca	ttggcaagac	tttggtgatg	180
accaggattg	gaattttata	aaaatattgt	tgatgggaag	ttgctaaagg	gtgaattact	240
tccctcagaa	gagtgtaaag	aaaagtcaga	gatgctataa	tagcagctat	tttaattggc	300
aagtgccact	gtggaaagag	ttcctgtgtg	tgctgaagtt	ctgaagggca	gtcaaattca	360
tcagcatggg	ctgtttgggtg	caaatgcaaa	agcacaggtc	tttttagcat	gctgggtctct	420
cccgtgtcct	tatgcaaata	atcgtcttct	tctaaatttc	tcctaggctt	cattttccaa	480
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<210> 343

<211> 382

<212> DNA

<213> Homo sapien

<400> 343

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aaaccacca	gctgaaaaaa	aa				382

<210> 344

<211> 536

<212> DNA

<213> Homo sapien

<400> 344

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<210> 345

<211> 251

<212> DNA

<213> Homo sapien

<400> 345

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gcgtagggcca ggaaatcaca tctacactg cccaggagcc agacacattt atggaacaga      180
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<210> 346

<211> 282

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

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<223> n = A,T,C or G

<400> 346

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agaaaggctt tctatttcac tggcccaggt agggggaagg agagtaactt tgagtctgtg      240
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<210> 347

<211> 201

<212> DNA

<213> Homo sapien

<220>

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<223> n = A,T,C or G

<400> 347

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<210> 348

<211> 251

<212> DNA

<213> Homo sapien

<400> 348

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aggagacact cccagcatgg aggagggtt atcttttcat ctaggtcag gtctacaatg      180
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<210> 349

<211> 251

<212> DNA

<213> Homo sapien

<400> 349

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cagaagggtc tgaactctac	gtgttaccag	agaacataat	gcaattcatg	cattccactt	180
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<210> 350

<211> 908

<212> DNA

<213> Homo sapien

<400> 350

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tatcaatatg caggagccat	cttgcagggt	tgatgctggt	tatactggac	aacactgtga	840
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<210> 351

<211> 472

<212> DNA

<213> Homo sapien

<400> 351

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cattaacttg attttaaaat	cagwtttgyg	agtcatttac	cacaagctaa	atgtgtacac	180
tatgataaaa acaaccattg	tattcctggt	tttctaaaca	gtcctaattt	ctaactgt	240
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gatctgtcca caacaaactt	gccctctcat	gccttgctc	tcaccatgct	ctgctccagg	360
tcagccccct tttggcctgt	ttgtttgtc	aaaaacctaa	tctgcttctt	gcttttcttg	420
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<210> 352

<211> 251

<212> DNA

<213> Homo sapien

<400> 352

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caggctgcgt tccgtcctta	cgatgaagac	cacgatgcag	tttccaaaca	ttgccactac	180
atacatggaa aggaggggga	agccaaccca	gaaatgggct	ttctctaatac	ctgggatacc	240
aataagcaca a					251

<210> 353
 <211> 436
 <212> DNA
 <213> Homo sapien

<400> 353
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 cacattatgg tattattact atactgatta tatttatcat gtgacttcta attaaaaaat 120
 gtatccaaaa gcaaaacagc agatatacaa aattaaagag acagaagata gacattaaca 180
 gataaggcaa cttatacatt gacaatccaa atccaatata tttaaacatt tgggaaatga 240
 gggggacaaa tggaagccar atcaaatttg tgtaaaacta ttcagtatgt ttcccttgct 300
 tcatgtctga raaggctctc ccttcaatgg ggatgacaaa ctccaaatgc cacacaaatg 360
 ttaacagaat actagattca cactggaacg ggggtaaaga agaaattatt ttctataaaa 420
 gggctcctaa tgtagt 436

<210> 354
 <211> 854
 <212> DNA
 <213> Homo sapien

<400> 354
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 atcagggacc accctttggg ttgatatttt gcttaatctg catcttttga gtaagatcat 180
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 atatcaactg cataaatgta aaatgcatgt gacccaagaa ggccccaag tggcagacaa 780
 cattgtacct attttccctt ccaaaatgtg agcggcgggc ctgctgcttt caaggctgtc 840
 acacgggatg tcag 854

<210> 355
 <211> 676
 <212> DNA
 <213> Homo sapien

<400> 355
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 atccacaagt catacctgga tgtcagcgaa gagggcacgg aggcagcagc agccactggg 180
 gacagcatcg ctgtaaaaag cctaccaatg agagctcagt tcaaggcgaa ccacccttc 240
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 ccctaactcag atggggttga gtaaggctca gagggtgcaga tgaggtgcag agacaatcct 360
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 tcatctgcaa aatagggtcta ggatttcttc caaccatttc atgagttgtg aagctaaggc 480
 tttgttaatc atggaaaaag gtagacttat gcagaaagcc tttctggctt tcttatctgt 540
 ggtgtctcat ttgagtgtc tccagtgaca tgatcaagtc aatgagtaaa attttaaggg 600
 attagatttt ctgacttgt atgtatctgt gagatcttga ataagtgacc tgacatctct 660
 gcttaaagaa aaccag 676

<210> 356

<211> 574
 <212> DNA
 <213> Homo sapien

<400> 356
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 caagcttccc atttgtagat ctgagtgccat atgagtatct gacacctgtt cctctcttca 180
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 agatacaagc tcgtttacat gtgatagatc taacaaaggc atctaccgaa gtctggtctg 480
 gatagacggc acaggagct cttagggtcag cgctgctggg tggaggacat tcctgagtcc 540
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<210> 357
 <211> 393
 <212> DNA
 <213> Homo sapien

<400> 357
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 aagccacaac caaracttga tttatcaaac aaaaaccctt aaatataaac ggsaaaaaag 180
 atagatataa ttattccagt ttttttaaaa cttaaaarat attccattgc cgaattaara 240
 araarataag tggttatatg aaagaagggc attcaagcac actaaaraaa cctgaggkaa 300
 gcataatctg tacaaaatta aactgtcctt tttggcattt taacaaattt gcaacgktct 360
 ttttttctt tttctgtttt tttttttttt tac 393

<210> 358
 <211> 630
 <212> DNA
 <213> Homo sapien

<400> 358
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 gcatagagta gggaagctaa tccagcacag ggaggtcaca gagacatccc taagggaagtg 180
 gagttaaac ttgagaagc aagtgcctaa actgaaggat gtgttgaaaga agaagggaga 240
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 tcaactgaagg gagtaatgtg acattacttt tcaactcagg atggccattc taactccagg 480
 gggtagactg gactaggtaa gactggaggc aggtagacct cttctaaggc ctgcgatagt 540
 gaaagacaaa aataagtggg gaaattcagg ggatagtga aatcagtagg acttaatgag 600
 caagccagag gttcctccac aacaaccagt 630

<210> 359
 <211> 620
 <212> DNA
 <213> Homo sapien

<400> 359
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 ctaccagaa gaataaagtg ctctgccagt tattaaagga ttactgctgg tgaattaaat 180
 atggcattcc ccaagggaaa tagagagatt cttctggatt atgttcaata tttattttac 240

aggattaact	gttttaggaa	cagatataaa	gcttcgccac	ggaagagatg	gacaaagcac	300
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tgcaacatta	tgcttcatga	ataatatgta	gaaagaaggt	ctgatgaaaa	tgacatcctt	420
aatgtaagat	aactttataa	gaattctggg	tcaaataaaa	ttctttgaag	aaaacatcca	480
aatgtcattg	actttatcaa	tactatcttg	gcatataacc	tatgaaggca	aaactaaaca	540
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ctgtaaagat	gtgacagtgt					620

<210> 360
 <211> 431
 <212> DNA
 <213> Homo sapien

<400> 360						
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tactcatcat	ttttggccag	cagttgtttg	atcaccaaac	atcatgccag	aatactcagc	180
aaaccttctt	agctcttgag	aagtcaaagt	ccgggggaat	ttattcctgg	caattttaat	240
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agtggacatg	cagtggcaga	gctcctggta	accacctaga	ggaatacaca	ggcacatgtg	360
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<210> 361
 <211> 351
 <212> DNA
 <213> Homo sapien

<400> 361						
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<210> 362
 <211> 463
 <212> DNA
 <213> Homo sapien

<400> 362						
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ccccggtcac	agaaatgacc	aggttgggtg	ttttcagggt	ccagtgctgg	gtcagcagct	180
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cacacttgca	cacattctcc	ctgataagca	cgatgggtgtg	gacaggaagg	aaggatttca	420
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<210> 363
 <211> 653
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature

<222> (1)...(653)

<223> n = A,T,C or G

<400> 363

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<210> 364

<211> 401

<212> DNA

<213> Homo sapien

<400> 364

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aaaacaaggt	ggatagatct	agaattgtaa	catttttaaga	aaaccatagc	atttgacaga	180
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acgtgcatag	taaatcttta	tatttgctat	ggcgttgac	tagaggactt	ggactgcaac	360
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<210> 365

<211> 356

<212> DNA

<213> Homo sapien

<400> 365

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<210> 366

<211> 1851

<212> DNA

<213> Homo sapien

<400> 366

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<210> 367

<211> 668

<212> DNA

<213> Homo sapien

<400> 367

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accrtataag	agcagtgtct	tggccattaa	tttatctttc	attrtagaca	gcrtagtgya	180
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<210> 368

<211> 1512

<212> DNA

<213> Homo sapien

<400> 368

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ggagaccacg	acgactctgc	tatgaagaca	ctcaggagca	agatgggcaa	gtgggtccgc	420
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gacgaytctg	ctatgaagac	actcaggaac	aagatgggca	agtgggtgctg	ccactgcttc	540
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<210> 369

<211> 1853

<212> DNA

<213> Homo sapien

<400> 369

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<210> 370

<211> 2184

<212> DNA

<213> Homo sapien

<400> 370

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<210> 371

<211> 1855

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

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<400> 371

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<210> 372

<211> 1059

<212> DNA

<213> Homo sapien

<400> 372

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<210> 373

<211> 1155

<212> DNA

<213> Homo sapien

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<211> 2000

<212> DNA

<213> Homo sapien

<400> 374

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 <213> Homo sapien

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 aagcatgaaa gtaataatgt gggattacta gaaaacctga ctaatggtgt cactgctggc 1320
 aatggtgata atggattaat tcctcaaagg aagagcagaa cacctgaaaa tcagcaattt 1380
 cctgacaacg aaagtgaaga gtatcacaga atttgcgaat tagtttctga ctacaaagaa 1440
 aaacagatgc caaaatactc ttctgaaaac agcaaccacg aacaagactt aaagctgaca 1500
 tcagaggaag agtcacaaag gcttgagggc agtgaaaaatg gccagccaga gaaaagatct 1560
 caagaaccag aaataaataa ggatggtgat agagagctag aaaattttat ggctatcgaa 1620
 gaaatgaaga agcaggaag tactcatgtc ggattcccag aaaacctgac taatggtgcc 1680
 actgctggca atggtgatga tggattaatt cctccaagga agagcagaac acctgaaagc 1740
 cagcaatttc ctgacactga gaatgaagag tatcacagt acgaacaaaa tgatactcag 1800
 aagcaatttt gtgaagaaca gaacactgga atattacacg atgagattct gattcatgaa 1860
 gaaaagcaga tagaagtggg tgaaaaaatg aattctgagc tttctcttag ttgtaagaaa 1920
 gaaaagaca tcttgcataa aaatagtagc ttgcgggaag aaattgccat gctaagactg 1980
 gagctagaca caatgaaaca tcagagccag ctaaaaaaa aaaaaaaaaa aaaaaaaaaa 2040

<210> 376
 <211> 329
 <212> PRT
 <213> Homo sapien

<400> 376
 Met Asp Ile Val Ser Gly Ser His Pro Leu Trp Val Asp Ser Phe
 1 5 10 15
 Leu His Leu Ala Gly Ser Asp Leu Leu Ser Arg Ser Leu Met Ala Glu
 20 25 30
 Glu Tyr Thr Ile Val His Ala Ser Phe Ile Ser Cys Ile Ser Ser Ser
 35 40 45
 Leu Asp Gly Gln Gly Glu Arg Gln Glu Gln Arg Gly His Phe Trp Arg
 50 55 60

```

Pro Gln Arg Leu Leu Cys Glu Asp Ala Trp Glu Gln Glu Val Gln Val
65          70          75          80
Val Leu Pro Leu Leu Pro Leu Leu Gln Gly Ser Gly Lys Ser Asn Val
          85          90          95
Val Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr
          100          105          110
His Val His Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp
          115          120          125
Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp
          130          135          140
Val Asn Lys Arg Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser
145          150          155          160
Ala Asn Gly Asn Ser Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys
          165          170          175
Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala
          180          185          190
Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly
          195          200          205
Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr
          210          215          220
Ala Val Tyr Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr
225          230          235          240
Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu
          245          250          255
Leu Gly Ile His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys
          260          265          270
Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu
          275          280          285
Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu
290          295          300
Glu Gln Asn Val Asp Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu
305          310          315          320
Ser Met Leu Phe Leu Val Ile Ile Met
          325

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<210> 377

<211> 148

<212> PRT

<213> Homo sapien

<220>

<221> VARIANT

<222> (1)...(148)

<223> Xaa = Any Amino Acid

<400> 377

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Met Thr Xaa Pro Ser Trp Ser Pro Gly Thr Thr Ser Val Glu Lys Ile
1          5          10          15
Trp Thr Ser Ser Thr Glu Leu Pro Trp Trp Gly Lys Val Pro Arg Lys
          20          25          30
Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Xaa Asp Lys
          35          40          45
Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu
          50          55          60
Val Val Lys Leu Xaa Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp
65          70          75          80
Asn Lys Lys Arg Thr Ala Leu Xaa Lys Ala Val Gln Cys Gln Glu Asp
          85          90          95

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Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro
 100 105 110
 Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Xaa Tyr Asn Glu Asp
 115 120 125
 Lys Leu Met Ala Lys Ala Leu Leu Tyr Gly Ala Asp Ile Glu Ser
 130 135 140
 Lys Asn Lys Val
 145

<210> 378
 <211> 1719
 <212> PRT
 <213> Homo sapien

<400> 378
 Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
 1 5 10 15
 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
 20 25 30
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val

			340					345					350			
Ile	Cys	Gln	Leu	Leu	Ser	Asp	Tyr	Lys	Glu	Lys	Gln	Met	Leu	Lys	Ile	
		355					360					365				
Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu	Asn	Val	Ser	Arg	Thr	Arg	Asn	Lys	
		370				375					380					
Pro	Arg	Thr	His	Met	Val	Val	Glu	Val	Asp	Ser	Met	Pro	Ala	Ala	Ser	
385					390					395					400	
Ser	Val	Lys	Lys	Pro	Phe	Gly	Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp	Cys	
				405				410						415		
Cys	Arg	Cys	Phe	Pro	Cys	Cys	Arg	Glu	Ser	Gly	Lys	Ser	Asn	Val	Gly	
			420					425				430				
Thr	Ser	Gly	Asp	His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Ser	Lys	
		435				440						445				
Met	Gly	Lys	Trp	Cys	Arg	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser	Gly	
		450				455					460					
Lys	Ser	Asn	Val	Gly	Ala	Ser	Gly	Asp	His	Asp	Ser	Ala	Met	Lys		
465					470					475					480	
Thr	Leu	Arg	Asn	Lys	Met	Gly	Lys	Trp	Cys	Cys	His	Cys	Phe	Pro	Cys	
				485				490						495		
Cys	Arg	Gly	Ser	Gly	Lys	Ser	Lys	Val	Gly	Ala	Trp	Gly	Asp	Tyr	Asp	
			500					505				510				
Asp	Ser	Ala	Phe	Met	Glu	Pro	Arg	Tyr	His	Val	Arg	Gly	Glu	Asp	Leu	
		515				520						525				
Asp	Lys	Leu	His	Arg	Ala	Ala	Trp	Trp	Gly	Lys	Val	Pro	Arg	Lys	Asp	
		530				535					540					
Leu	Ile	Val	Met	Leu	Arg	Asp	Thr	Asp	Val	Asn	Lys	Lys	Asp	Lys	Gln	
545					550					555					560	
Lys	Arg	Thr	Ala	Leu	His	Leu	Ala	Ser	Ala	Asn	Gly	Asn	Ser	Glu	Val	
				565				570						575		
Val	Lys	Leu	Leu	Leu	Asp	Arg	Arg	Cys	Gln	Leu	Asn	Val	Leu	Asp	Asn	
			580					585				590				
Lys	Lys	Arg	Thr	Ala	Leu	Ile	Lys	Ala	Val	Gln	Cys	Gln	Glu	Asp	Glu	
		595					600					605				
Cys	Ala	Leu	Met	Leu	Leu	Glu	His	Gly	Thr	Asp	Pro	Asn	Ile	Pro	Asp	
		610				615					620					
Glu	Tyr	Gly	Asn	Thr	Thr	Leu	His	Tyr	Ala	Ile	Tyr	Asn	Glu	Asp	Lys	
625					630					635					640	
Leu	Met	Ala	Lys	Ala	Leu	Leu	Leu	Tyr	Gly	Ala	Asp	Ile	Glu	Ser	Lys	
				645					650					655		
Asn	Lys	His	Gly	Leu	Thr	Pro	Leu	Leu	Leu	Gly	Val	His	Glu	Gln	Lys	
			660					665					670			
Gln	Gln	Val	Val	Lys	Phe	Leu	Ile	Lys	Lys	Lys	Ala	Asn	Leu	Asn	Ala	
		675					680					685				
Leu	Asp	Arg	Tyr	Gly	Arg	Thr	Ala	Leu	Ile	Leu	Ala	Val	Cys	Cys	Gly	
						695										

				805				810				815			
Leu	Leu	Glu	Asn	Leu	Thr	Asn	Gly	Val	Thr	Ala	Gly	Asn	Gly	Asp	Asn
820				840				825				830			
Gly	Leu	Ile	Pro	Gln	Arg	Lys	Ser	Arg	Thr	Pro	Glu	Asn	Gln	Gln	Phe
835				855				845				860			
Pro	Asp	Asn	Glu	Ser	Glu	Glu	Tyr	His	Arg	Ile	Cys	Glu	Leu	Val	Ser
850				870				875				880			
Asp	Tyr	Lys	Glu	Lys	Gln	Met	Pro	Lys	Tyr	Ser	Ser	Glu	Asn	Ser	Asn
865				885				890				895			
Pro	Glu	Gln	Asp	Leu	Lys	Leu	Thr	Ser	Glu	Glu	Glu	Ser	Gln	Arg	Leu
900				905				910				915			
Glu	Gly	Ser	Glu	Asn	Gly	Gln	Pro	Glu	Leu	Glu	Asn	Phe	Met	Ala	Ile
915				920				925				930			
Glu	Glu	Met	Lys	Lys	His	Gly	Ser	Thr	His	Val	Gly	Phe	Pro	Glu	Asn
930				935				940				945			
Leu	Thr	Asn	Gly	Ala	Thr	Ala	Gly	Asn	Gly	Asp	Asp	Gly	Leu	Ile	Pro
945				950				955				960			
Pro	Arg	Lys	Ser	Arg	Thr	Pro	Glu	Ser	Gln	Gln	Phe	Pro	Asp	Thr	Glu
955				965				970				975			
Asn	Glu	Glu	Tyr	His	Ser	Asp	Glu	Gln	Asn	Asp	Thr	Gln	Lys	Gln	Phe
980				985				990				995			
Cys	Glu	Glu	Gln	Asn	Thr	Gly	Ile	Leu	His	Asp	Glu	Ile	Leu	Ile	His
995				1000				1005				1010			
Glu	Glu	Lys	Gln	Ile	Glu	Val	Val	Glu	Lys	Met	Asn	Ser	Glu	Leu	Ser
1010				1015				1020				1025			
Leu	Ser	Cys	Lys	Lys	Glu	Lys	Asp	Ile	Leu	His	Glu	Asn	Ser	Thr	Leu
1025				1030				1035				1040			
Arg	Glu	Glu	Ile	Ala	Met	Leu	Arg	Leu	Glu	Leu	Asp	Thr	Met	Lys	His
1045				1050				1055				1060			
Gln	Ser	Gln	Leu	Pro	Arg	Thr	His	Met	Val	Val	Glu	Val	Asp	Ser	Met
1060				1065				1070				1075			
Pro	Ala	Ala	Ser	Ser	Val	Lys	Lys	Pro	Phe	Gly	Leu	Arg	Ser	Lys	Met
1075				1080				1085				1090			
Gly	Lys	Trp	Cys	Cys	Arg	Cys	Phe	Pro	Cys	Cys	Arg	Glu	Ser	Gly	Lys
1090				1095				1100				1105			
Ser	Asn	Val	Gly	Thr	Ser	Gly	Asp	His	Asp	Asp	Ser	Ala	Met	Lys	Thr
1105				1110				1115				1120			
Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp	Cys	Arg	His	Cys	Phe	Pro	Cys	Cys
1125				1130				1135				1140			
Arg	Gly	Ser	Gly	Lys	Ser	Asn	Val	Gly	Ala	Ser	Gly	Asp	His	Asp	Asp
1140				1145				1150				1155			
Ser	Ala	Met	Lys	Thr	Leu	Arg	Asn	Lys	Met	Gly	Lys	Trp	Cys	Cys	His
1155				1160				1165				1170			
Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser	Gly	Lys	Ser	Lys	Val	Gly	Ala	Trp
1170				1175				1180				1185			
Gly	Asp	Tyr	Asp	Asp	Ser	Ala	Phe	Met	Glu	Pro	Arg	Tyr	His	Val	Arg
1185				1190				1195				1200			
Gly	Glu	Asp	Leu	Asp	Lys	Leu	His	Arg	Ala	Ala	Trp	Trp	Gly	Lys	Val
1205				1210				1215				1220			
Pro															

1265 1270 1275 1280
 Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr
 1285 1290 1295
 Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp
 1300 1305 1310
 Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val
 1315 1320 1325
 His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala
 1330 1335 1340
 Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala
 1345 1350 1355 1360
 Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn
 1365 1370 1375
 Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr
 1380 1385 1390
 Ala Val Ser Ser His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr
 1395 1400 1405
 Lys Glu Lys Lys Gln Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu
 1410 1415 1420
 Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly
 1425 1430 1435 1440
 Ser Glu Asn Ser Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn
 1445 1450 1455
 Lys Asp Gly Asp Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser
 1460 1465 1470
 Asn Asn Val Gly Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly
 1475 1480 1485
 Asn Gly Asp Asn Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu
 1490 1495 1500
 Asn Gln Gln Phe Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys
 1505 1510 1515 1520
 Glu Leu Val Ser Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser
 1525 1530 1535
 Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu
 1540 1545 1550
 Ser Gln Arg Leu Glu Gly Ser Glu Asn Gly Gln Pro Glu Lys Arg Ser
 1555 1560 1565
 Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Leu Glu Asn Phe
 1570 1575 1580
 Met Ala Ile Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe
 1585 1590 1595 1600
 Pro Glu Asn Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly
 1605 1610 1615
 Leu Ile Pro Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro
 1620 1625 1630
 Asp Thr Glu Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln
 1635 1640 1645
 Lys Gln Phe Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile
 1650 1655 1660
 Leu Ile His Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser
 1665 1670 1675 1680
 Glu Leu Ser Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn
 1685 1690 1695
 Ser Thr Leu Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr
 1700 1705 1710
 Met Lys His Gln Ser Gln Leu
 1715

<210> 379
 <211> 656
 <212> PRT
 <213> Homo sapien

<400> 379
 Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
 1 5 10 15
 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
 20 25 30
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
 340 345 350
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
 355 360 365
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu
 370 375 380
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys
 385 390 395 400
 Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu
 405 410 415

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<210> 380
<211> 671
<212> PRT
<213> Homo sapien
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<400> 380															
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Pro	Phe	Gly	Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp	Cys	Cys	Arg	Cys	Phe
			20					25					30		
Pro	Cys	Cys	Arg	Glu	Ser	Gly	Lys	Ser	Asn	Val	Gly	Thr	Ser	Gly	Asp
		35					40					45			
His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp
	50					55					60				
Cys	Arg	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser	Gly	Lys	Ser	Asn	Val
65					70					75				80	
Gly	Ala	Ser	Gly	Asp	His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Asn
				85					90					95	
Lys	Met	Gly	Lys	Trp	Cys	Cys	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser
			100					105					110		
Gly	Lys	Ser	Lys	Val	Gly	Ala	Trp	Gly	Asp	Tyr	Asp	Asp	Ser	Ala	Phe
		115					120					125			
Met	Glu	Pro	Arg	Tyr	His	Val	Arg	Gly	Glu	Asp	Leu	Asp	Lys	Leu	His
	130					135					140				
Arg	Ala	Ala	Trp	Trp	Gly	Lys	Val	Pro	Arg	Lys	Asp	Leu	Ile	Val	Met
145					150					155				160	
Leu	Arg	Asp	Thr	Asp	Val	Asn	Lys	Lys	Asp	Lys	Gln	Lys	Arg	Thr	Ala

					165					170					175
Leu	His	Leu	Ala	Ser	Ala	Asn	Gly	Asn	Ser	Glu	Val	Val	Lys	Leu	Leu
			180					185					190		
Leu	Asp	Arg	Arg	Cys	Gln	Leu	Asn	Val	Leu	Asp	Asn	Lys	Lys	Arg	Thr
		195					200					205			
Ala	Leu	Ile	Lys	Ala	Val	Gln	Cys	Gln	Glu	Asp	Glu	Cys	Ala	Leu	Met
		210				215					220				
Leu	Leu	Glu	His	Gly	Thr	Asp	Pro	Asn	Ile	Pro	Asp	Glu	Tyr	Gly	Asn
225					230					235					240
Thr	Thr	Leu	His	Tyr	Ala	Ile	Tyr	Asn	Glu	Asp	Lys	Leu	Met	Ala	Lys
				245					250					255	
Ala	Leu	Leu	Leu	Tyr	Gly	Ala	Asp	Ile	Glu	Ser	Lys	Asn	Lys	His	Gly
			260					265					270		
Leu	Thr	Pro	Leu	Leu	Leu	Gly	Val	His	Glu	Gln	Lys	Gln	Gln	Val	Val
		275					280					285			
Lys	Phe	Leu	Ile	Lys	Lys	Lys	Ala	Asn	Leu	Asn	Ala	Leu	Asp	Arg	Tyr
		290				295					300				
Gly	Arg	Thr	Ala	Leu	Ile	Leu	Ala	Val	Cys	Cys	Gly	Ser	Ala	Ser	Ile
305					310					315					320
Val	Ser	Leu	Leu	Leu	Glu	Gln	Asn	Ile	Asp	Val	Ser	Ser	Gln	Asp	Leu
				325					330					335	
Ser	Gly	Gln	Thr	Ala	Arg	Glu	Tyr	Ala	Val	Ser	Ser	His	His	His	Val
			340					345					350		
Ile	Cys	Gln	Leu	Leu	Ser	Asp	Tyr	Lys	Glu	Lys	Gln	Met	Leu	Lys	Ile
		355					360					365			
Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu	Gln	Asp	Leu	Lys	Leu	Thr	Ser	Glu
		370				375					380				
Glu	Glu	Ser	Gln	Arg	Phe	Lys	Gly	Ser	Glu	Asn	Ser	Gln	Pro	Glu	Lys
385					390					395					400
Met	Ser	Gln	Glu	Pro	Glu	Ile	Asn	Lys	Asp	Gly	Asp	Arg	Glu	Val	Glu
				405					410					415	
Glu	Glu	Met	Lys	Lys	His	Glu	Ser	Asn	Asn	Val	Gly	Leu	Leu	Glu	Asn
			420					425					430		
Leu	Thr	Asn	Gly	Val	Thr	Ala	Gly	Asn	Gly	Asp	Asn	Gly	Leu	Ile	Pro
		435					440					445			
Gln	Arg	Lys	Ser	Arg	Thr	Pro	Glu	Asn	Gln	Gln	Phe	Pro	Asp	Asn	Glu
					455						460				
Ser	Glu	Glu	Tyr	His	Arg	Ile	Cys	Glu	Leu	Val	Ser	Asp	Tyr	Lys	Glu
465					470					475					480
Lys	Gln	Met	Pro	Lys	Tyr	Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu	Gln	Asp
				485					490					495	
Leu	Lys	Leu	Thr	Ser	Glu	Glu	Glu	Ser	Gln	Arg	Leu	Glu	Gly	Ser	Glu
			500					505					510		
Asn	Gly	Gln	Pro	Glu	Lys	Arg	Ser	Gln	Glu	Pro	Glu	Ile	Asn	Lys	Asp
		515													

625		630		635		640
Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile Ala						
		645		650		655
Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu						
	660		665		670	

<210> 381

<211> 251

<212> DNA

<213> Homo sapien

<400> 381

ggagaagcgt	ctgctggggc	aggaaggggt	ttccctgcc	tctcacctgt	ccctcaccaa	60
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ccaatatccc	aggagaagca	ttggggagtt	gggggcaggt	gaaggacca	ggactcacac	180
atcctggggc	tccaaggcag	aggagagggt	cctcaagaag	gtcaggagga	aaatccgtaa	240
caagcagtca	g					251

<210> 382

<211> 3279

<212> DNA

<213> Homo sapiens

<400> 382

cttcctgcag	cccccatgct	ggtgaggggc	acgggcagga	acagtggacc	caacatggaa	60
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cactgggagg	ggacatcctg	cagaaggtag	gagttagcaa	acaccgctg	caggggaggg	180
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cagggcgcgga	gatggcctca	cacaggggaag	agagggcccc	tcctgcaggg	cctcacctgg	360
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cgtcagattt	gatgatttcc	tagcaggact	tacagaaata	aagagctatc	atgctgtggt	1920
ttattatggt	ttgttacatt	gataggatac	atactgaaat	cagcaaacaa	aacagatgta	1980
tagattagag	tgtggagaaa	acagaggaaa	acttgcagtt	acgaagactg	gcaacttggc	2040

```

tttactaagt tttcagactg gcaggaagtc aaacctatta ggctgaggac cttgtggagt 2100
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gcatatccga cagttattct ctccaagtgg agacttacgg acagcatata attctccctg 2220
caaggatgta tgataatatg tacaaagtaa ttccaactga ggaagctcac ctgaccccta 2280
gtgtccaggg tttttactgg ggggtctgtag gacgagtatg gagtacttga ataattgacc 2340
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cccagctgat agaggaagta gccaggtggg agcctttccc agtgggtgtg ggacatatct 3180
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gttttcagac cttaaaaaaa aaaaaaaaaa aaaagtttt 3279

```

<210> 383

<211> 154

<212> PRT

<213> Homo sapiens

<400> 383

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Gly Lys Arg Gly Pro Leu Leu Gln Gly Leu Thr Trp Ala Thr Gly Gly
      20                      25                      30

His Cys Phe Ser Ser Glu Glu Ser Gly Ala Val Asp Gly Ala Gly Gln
      35                      40                      45

Lys Lys Asp Arg Ala Trp Leu Arg Cys Pro Glu Ala Val Ala Gly Phe
      50                      55                      60

Pro Leu Gly Ser Asp Cys Arg Glu Gly Gly Arg Gln Gly Cys Gly Gly
      65                      70                      75                      80

Ser Asp Asp Glu Asp Asp Leu Gly Val Ala Pro Gly Leu Ala Pro Ala
      85                      90                      95

Trp Ala Leu Thr Gln Pro Pro Ser Gln Ser Pro Gly Pro Gln Ser Leu
      100                     105                     110

Pro Ser Thr Pro Ser Ser Ile Trp Pro Gln Trp Val Ile Leu Ile Thr
      115                     120                     125

Glu Leu Thr Ile Pro Ser Pro Ala His Gly Pro Pro Trp Leu Pro Asn
      130                     135                     140

Ala Leu Glu Arg Gly His Leu Val Arg Glu
      145                     150

```

<210> 384
<211> 557
<212> DNA
<213> Homo sapiens

<400> 384
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ggggaagggt ccccttttgc ttgccaagtg ccataaccat gagcactact ctaccatggg 180
tctgcctcct ggccaagcag gctggtttgc aagaatgaaa tgaatgattc tacagctagg 240
acttaacctt gaaatggaaa gtcttgcaat cccatttgca ggatccgtct gtgcacatgc 300
ctctgtagag agcagcattc ccagggacct tggaaacagt tggcactgta aggtgcttgc 360
tccccaagac acatcctaaa aggtgttgta atggtgaaaa cgtcttcctt ctttattgcc 420
ccttcttatt tatgtgaaca actgtttgtc tttttttgta tcttttttaa actgtaaagt 480
tcaattgtga aatgaatat catgcaaata aattatgcga ttttttttcc aaagtaaaaa 540
aaaaaaaaaa aaaaaaa 557

<210> 385
<211> 337
<212> DNA
<213> Homo sapiens

<400> 385
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gtttctctag cagcagatgg gttaggagga agtgacccaa gtggttgact cctatgtgca 120
tctcaaagcc atctgctgtc ttcgagtacg gacacatcat cactcctgca ttgttgatca 180
aaacgtggag gtgcttttcc tcagctaaga agcccttagc aaaagctcga atagacttag 240
tatcagacag gtccagtttc cgcaccaaca cctgctgggt ccctgtcgtg gtctggatct 300
ctttggccac caattcccc ttttccacat cccggca 337

<210> 386
<211> 300
<212> DNA
<213> Homo sapiens

<400> 386
gggcccgcta cgggccaggg ccccgccctcg cgagtccctcc tccccgggtg cctgcccgcga 60
gcccgctcgg cccagagggg gggcgcgggg ctgcctctac cggttgccgg ctgtaactca 120
gcgaccttgg cccgaaggct cttagcaagga cccaccgacc ccagccgcgg cggcgggcggc 180
gcggaacttg cccggtgtgt gggcgggagc ggactgctgt tccgcggacg ggcagcgaag 240
atgttagcct tcgctgccag gaccgtggac cgatcccagg gctgtggtgt aacctcagcc 300

<210> 387
<211> 537
<212> DNA
<213> Homo sapiens

<400> 387
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cccctcctg tgccatcatg atcagcacct atgagttcgg caaaagcttc ttccagaggc 120
tgaaccagga cggcttctg ggcggctgaa aggggcaagg aggcaaggac cccgtctctc 180
ccacggatgg ggagagggca ggaggagacc cagccaagtg ccttttctc agcactgagg 240
gagggggctt gtttcccttc cctcccggcg acaagctcca gggcagggtg gtccctctgg 300
gcggcccagc acctcctcag acacaacttc ttctgctgc tccagtcgtg gggatcatca 360
cttaccacc acccaagttc aagaccaa atctccagctg ccccttctgt gtttccctgt 420
gtttgtgtgta gctgggcatg tctccaggaa ccaagaagcc ctcagcctgg tgtagtctcc 480
ctgacccttg ttaattcctt aagtctaaag atgatgaact tcaaaaaaaaa aaaaaaa 537

<210> 388
<211> 520
<212> DNA
<213> Homo sapiens

<400> 388
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tgagggttaaa ccagtttgca ttcccctaata gtggaaaaag taaggaggact actcagcact 120
gtttgaagat tgcctcttct acagcttctg agaatttgtt tatttcactt gccaaagtga 180
ggacccccctc cccaacatgc cccagcccac ccctaagcat ggtcccttgt caccaggcaa 240
ccaggaaact gctacttgtg gacctcacca gagaccagga gggtttggtt agctcacagg 300
acttccccca cccagaaga ttagcatccc atactagact cataactcaac tcaactaggc 360
tcatactcaa ttgatggta ttagacaatt ccatttctt ctggttatta taaacagaaa 420
atctttcttc ttctcattac cagtaaaggc tcttggtatc tttctggttg aatgatttct 480
atgaacttgt cttattttta tgggtgggtt ttttctgtgt 520

<210> 389
<211> 365
<212> DNA
<213> Homo sapiens

<400> 389
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aacgactttc caaataatct caccagcgcc ttccagctca ggcgtcctag aagcgtcttg 180
aagcctatgg ccagctgtct ttgtgttccc tctcaccgc ctgtcctcac agctgagact 240
cccaggaaac cttcagacta ctttctctg cttcagcaa ggggcgttgc ccacattctc 300
tgagggtcag tggaagaacc tagactccca ttgctagagg tagaaagggg aagggtgctg 360
gggag 365

<210> 390
<211> 221
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(221)
<223> n = A,T,C or G

<400> 390
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tacacggntt ctcattgggtg tggaacatct ctgcttgccg tttcaggaag gcctctggct 120
gctctangag tctgancga ntcgttgccc cantntgaca naaggaaagg cggagcttat 180
tcaaagtcta gagggtgtg aggagttaag gctggatttc a 221

<210> 391
<211> 325
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(325)
<223> n = A,T,C or G

<400> 391


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tggagcaggt cccgaggcct ccctagagcc tggggccgac tctgtgncga tgcangcttt 60
ctctcgcgcc cagcctggag ctgctcctgg catctacca caatcagncg aggcgagcag 120
tagccagggc actgctgcca acagccagtc cnnataccat catgtnaccc ggtgngctct 180
naanttngat ntccanagcc ctacccatcn tagttctgct ctcccaccgg ntaccagccc 240
cactgcccag gaatcctaca gccagtaccc tgtcccgcg tctctaccta ccagtacgat 300
gagacctccg gctactacta tgacc                                     325

```

<210> 392

<211> 277

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(277)

<223> n = A,T,C or G

<400> 392

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atattgttta actccttcct ttatatcttt taacattttc atggngaaaag gttcacatct 60
agtctcactt nggcnagngn ctctactctg agtctcttcc ccggcctggn ccagtnngaa 120
antaccanga accgncatgn cttaanaacn nctgggtttn tgggttnntc aatgactgca 180
tgagtgacac caccctgtcc actacgtgat gctgtaggat taaagtctca cagtggggcg 240
ctgaggatac agcgccgcgt cctgtgttgc tgggggaa                                     277

```

<210> 393

<211> 566

<212> DNA

<213> Homo sapiens

<400> 393

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actagtcacg tgtggtggaa ttcgcgcccg cgtcgacgga caggtcagct gtctggctca 60
gtgatctaca ttctgaagtt gtctgaaaat gtcttcatga tttaaattcag cctaaacggt 120
ttgccgggaa cactgcagag acaatgctgt gagtttccaa ccttagccca tctgcgggca 180
gagaaggtct agtttgcca tcagcattat catgatatca ggactgggta cttgggttaag 240
gaggggtcta ggagatctgt cccttttaga gacaccttac ttataatgaa gtatttgga 300
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catttattaa tcatccctgc ctgtgtctat tattatatc atatctctac gctggaaact 420
ttctgectca atgtttactg tgcccttgtt tttgctagtt tgtgttgttg aaaaaaaaaa 480
cattctctgc ctgagtttta atttttgc cc aaagtattt taatctatac aattaaaagc 540
ttttgcctat caaaaaaaaaa aaaaaa                                     566

```

<210> 394

<211> 384

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(384)

<223> n = A,T,C or G

<400> 394

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gaacatacat gtcccggcac ctgagctgca gtctgacatc atcgccatca cgggcctcgc 60
tgcaaatng gaccgggcca aggctggact gctggagcgt gtgaaggagc tacaggccna 120
gcaggaggac cgggctttta ggagttttta gctgagtgct actgtagacc ccaaatacca 180
tcccaagatt atcgggagaa agggggcagt aattacccaa atccgggttg agcatgacgt 240
gaacatccag tttcctgata aggacgatgg gaaccagccc caggaccaa ttaccatcac 300
aggggtacgaa aagaacacag aagctgccag ggatgctata ctgagaattg tgggtgaact 360

```

tgagcagatg gtttctgagg acgt

384

<210> 395

<211> 399

<212> DNA

<213> Homo sapiens

<400> 395

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ggcaaaactg tgtgacctca ataagacctc gcagatccaa ggtcaagtat cagaagtgac 60
tctgaccttg gactccaaga cctacatcaa cagcctggct atattagatg atgagccagt 120
tatcagaggt ttcattcattg cggaaattgt ggagtctaag gaaatcatgg cctctgaagt 180
attcacgtct ttccagtacc ctgagttctc tatagagttg cctaacacag gcagaattgg 240
ccagctactt gtctgcaatt gtatcttcaa gaataccctg gccatccctt tgactgacgt 300
caagttctct ttggaaagcc tgggcatctc ctactacag acctctgacc atgggacggg 360
gcagcctggg gagaccatcc aatcccaaat aaaatgcac 399
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<210> 396

<211> 403

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(403)

<223> n = A,T,C or G

<400> 396

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gacattttca acttctgctc cagctgctga taaaacaaat catgtgttta gcttgactcc 120
agacaaggac aacctgttcc ttcataactc tctagagaaa aaaaggagtt gttagtagat 180
actaaaaaaaa gtggatgaat aatctggata tttttcctaa aaagattcct tgaaacacat 240
taggaaaatg gagggcctta tgatcagaat gctagaatta gtccattgtg ctgaagcagg 300
gtttaggggg gggagtgagg gataaaaagaa ggaaaaaaag aagagtgaga aaacctattt 360
atcaaagcag gtgctatcac tcaatgtagt gccctgctct ttt 403
```

<210> 397

<211> 100

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(100)

<223> n = A,T,C or G

<400> 397

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tccatccccg ctcttggttg gtnacagaat gactgacaaa 100
```

<210> 398

<211> 278

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(278)

<223> n = A,T,C or G

<400> 398

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gcggccgcgt cgacagcagt tccgccagcg ctgcccctg ggtgggggatg tgctgcacgc 60
ccacctggac atctggaagt cagcggcctg gatgaaagag cggacttcac ctggggcgat 120
tactactgt gcctcgacca gtgaggagag ctggaccgac agcgagggtg actcatcatg 180
ctccgggcag cccatccacc tgtggcagtt cctcaaggag ttgctactca agccccacag 240
ctatggccgc ttcattangt ggctcaacaa ggagaagg 278
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<210> 399

<211> 298

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(298)

<223> n = A,T,C or G

<400> 399

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acggagggtg aggaagcgnc cctgggatcg anaggatggg tcctgncatt gaccncctcn 60
ggggtgccng catggagcgc atgggcgcgg gcctgggcca cggcatggat cgcgtgggct 120
ccgagatcga gcgcatgggc ctggtcatgg accgcatggg ctccgtggag cgcgtgggct 180
ccggcattga gcgcatgggc ccgctgggccc tcgaccacat ggccctccanc attgancgca 240
tgggccagac catggagcgc attggctctg gcgtggagcn catgggtgcc ggcatggg 298
```

<210> 400

<211> 548

<212> DNA

<213> Homo sapiens

<400> 400

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acatcaacta cttcctcatt ttaaggatg gcagttccct tcatcccctt ttcctgcctt 60
gtacatgtac atgtatgaaa tttccttctc ttaccgaact ctctccacac atcacaaggt 120
caaagaacca cacgcttaga agggtaagag ggcaccctat gaaatgaaat ggtgatttct 180
tgagtctctt tttccacgt ttaaggggcc atggcaggac ttagagtgc gagttaagac 240
tgagaggggc tagagaatta tttcatacag gctttgaggc caccatgtc acttatcccg 300
tataccctct caccatcccc ttgtctactc tgatgcccc aagatgcaac tgggcagcta 360
gttgccccca taattctggg cctttgttgt ttgttttaat tacttgggca tcccaggaag 420
ctttccagtg atctcctacc atgggcccc ctcctgggat caagcccctc ccaggccctg 480
tccccagccc ctctgcccc agcccacccg cttgccttgg tgctcagccc tcccattggg 540
agcaggtt 548
```

<210> 401

<211> 355

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(355)

<223> n = A,T,C or G

<400> 401

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tgatgtctcc aagtagtcca ccttcattta actctttgaa actgtatcat ctttgccaag 120
taagagtggg ggcctatttc agctgctttg acaaaatgac tggctcctga cttaacgttc 180
tataaatgaa tgtgctgaag caaagtcccc atggtggcgg cgaagaagan aaagatgtgt 240
tttgttttgg actctctgtg gtcccttcca atgctgnngg tttccaacca ggggaagggt 300
```

cccttttgca ttgccaagtg ccataacctat gagcactact ctaccatggn tctgc 355

<210> 402

<211> 407

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(407)

<223> n = A,T,C or G

<400> 402

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tctcacatgc ggtggcatat ataggctcaa aataaaggaa tggagaaaaa tatttcaagc 120
aaatggaaaa cagaaaaaag cagggtgtgc actcctactt tctgacaaaa cagactatgc 180
gaataaagat aaaaaagaga aggacattac aaagggtggtc ctgacctttg ataaatctca 240
ttgcttgata ccaacctggg ctgttttaat tgcccaaacc aaaaggataa tttgctgagg 300
ttgtggagct tctcccctgc agagagtccc tgatctccca aaatttggtt gagatgtaag 360
gntgattttg ctgacaactc cttttctgaa gttttactca tttccaa 407
```

<210> 403

<211> 303

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(303)

<223> n = A,T,C or G

<400> 403

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tcctaagcaa gagccatggc atggtgaaaa tgcaaaagga gagtctggcc aatctacaaa 120
tagagaacaa gacctactca gtcataaaca aaaaggcaga caccaacatg gatctcatgg 180
gggattggat attgtaatta tagagcagga agatgacagt gatcgtcatt tggcacaaca 240
tcttaacaac gaccgaaacc cattatttac ataaacctcc attcggtaac catgttgaaa 300
gga 303
```

<210> 404

<211> 225

<212> DNA

<213> Homo sapiens

<400> 404

```
aagtgttaact tttaaaaatt tagtggattt tgaaaattct tagaggaaag taaaggaaaa 60
attgttaatg cactcattta cctttacatg gtgaaagtcc tctcttgatc ctacaacag 120
acattttcca ctctgttttc catagtgtgt aagtgtatca gatgtgttgg gcatgtgaat 180
ctccaagtgc ctgtgtaata aataaagtat ctttatttca ttcatt 225
```

<210> 405

<211> 334

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(334)

<223> n = A,T,C or G

<400> 405

```
gagctgttat actgtgagtt ctactaggaa atcatcaaat ctgagggttg tctggaggac 60
ttcaatacac ctccccccat agtgaatcag cttccagggg gtccagtcct tctccttact 120
tcatccccat cccatgccaa aggaagaccc tccctccttg gctcacagcc ttctctaggc 180
ttccagtgct ctccaggaca gagtgggtta tgttttcagc tccatccttg ctgtgagtgt 240
ctggtgcggt tgtgcctcca gcttctgctc agtgcttcat ggacagtgtc cagcccatgt 300
cactctccac tctctcannn tggatcccac ccct 334
```

<210> 406

<211> 216

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(216)

<223> n = A,T,C or G

<400> 406

```
tttcatacct aatgagggag ttganatnac atnnaaccag gaaatgcatg gatctcaang 60
gaaacaaaca cccaataaac tcggagtggc agactgacaa ctgtgagaca tgcacttgct 120
acnaaacaca aatttnatgt tgcacccttg tttctacacc tgtgggttat gacaaagaca 180
actgccaaag aatnttcaag aaggaggact gccant 216
```

<210> 407

<211> 413

<212> DNA

<213> Homo sapiens

<400> 407

```
gctgacttgc tagtatcatc tgcattcatt gaagcacaag aacttcatgc cttgactcat 60
gtaaatgcaa taggattaaa aaataaattt gatatcacat ggaaacagac aaaaaatatt 120
gtacaacatt gcacccagtg tcagattcta cacctggcca ctccaggaagc aagagttaat 180
cccagaggct tatgtcttaa tgtgttatgg caaatggatg tcatgcacgt accttcattt 240
ggaaaattgt catttgccta tgtgacagtt gatacttatt cacatttcat atgggcaacc 300
tgccagacag gagaaagtct tcccatgtta aaagacattt attatcttgt ttccctgtca 360
tgggagttcc agaaaaagtt aaaacagaca atgggccagg ttctgtagta aag 413
```

<210> 408

<211> 183

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(183)

<223> n = A,T,C or G

<400> 408

```
ggagctngcc ctcaattcct ccatntctat gttancatat ttaatgtctt ttgnnattaa 60
tncttaacta gttaatcctt aaagggttan ntaatcctta actagtcctt ccattgtgag 120
cattatcctt ccagtattcn ccttctnttt tatttactcc ttccctggcta cccatgtact 180
ntt 183
```

<210> 409

<211> 250

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(250)

<223> n = A,T,C or G

<400> 409

```
cccacgcatg ataagctctt tatttctgta agtcctgcta ggaaatcatc aaatctgacg 60
gtgggtttggg ggacctgaac aaacctcctg taattaatca gctttcagtt tctcccccta 120
gtccctcctt caacaacata ggaggatcct ccccttcttt ctgctcacgg ccttatctag 180
gcttcccagt gccccagga cagcgtgggc tatgtttaca gcgntcctt gctggggggg 240
ggccttatgc                                     250
```

<210> 410

<211> 306

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(306)

<223> n = A,T,C or G

<400> 410

```
ggctggtttg caagaatgaa atgaatgatt ctacagctag gacttaacct tgaaatggaa 60
agtcttgcaa tcccatttgc aggatccgtc tgtgcacatg cctctgtaga gagcagcatt 120
cccagggacc ttggaaacag ttggcactgt aagggtgctt ctccccaaga cacatcctaa 180
aagggtgtgt aatggtgaaa accgcttcct tctttattgc cccttcttat ttatgtgaac 240
nactggttgg ctttttttgn atctttttta aactggaaag ttcaattgng aaaatgaata 300
tctnctgc                                     306
```

<210> 411

<211> 261

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(261)

<223> n = A,T,C or G

<400> 411

```
agagatattn cttaggtnaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaagtgc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccocat cagttccagc 240
cttctctcaa ggngaggcaa a                                     261
```

<210> 412

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(241)

<223> n = A,T,C or G

<400> 412

```
gttcaatggt acctgacatt tctacaacac ccactcacc gatgtattcg ttgccagtg 60
ggaacatacc agcctgaatt tggaaaaaat aattgtgttt cttgccagc aaatactacg 120
actgacttttg atggctccac aaacataacc cagtgtaaaa acagaagatg tggaggggag 180
ctgggagatt tcaactggga cattgaattc ccaaactacc cangcaatta cccagccaac 240
a                                                                 241
```

<210> 413

<211> 231

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(231)

<223> n = A,T,C or G

<400> 413

```
aactcttaca atccaagtga ctcactgtg tgcttgaatc cttccactg tctcatctcc 60
ctcatecaag tttctagtac cttctctttg ttgtgaagga taatcaaac gaacaacaaa 120
aagtttactc tctcatttg gaacctaaaa actctcttct tctgggtct gagggctcca 180
agaatccttg aatcanttct cagatcattg gggacaccan atcaggaacc t          231
```

<210> 414

<211> 234

<212> DNA

<213> Homo sapiens

<400> 414

```
actgtccatg aagcactgag cagaagctgg aggcacaacg caccagacac tcacagcaag 60
gatggagctg aaaacataac ccactctgtc ctggaggcac tgggaagcct agagaaggct 120
gtgagccaag gagggagggt cttccttttg catgggatgg ggatgaagta aggagagggg 180
ctggaccccc tggaagctga ttcactatgg ggggagggtg attgaagtcc tcca      234
```

<210> 415

<211> 217

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(217)

<223> n = A,T,C or G

<400> 415

```
gcataggatt aagactgagt atcttttcta cattctttta actttctaag gggcacttct 60
caaaacacag accaggtagc aaatctccac tgctctaagg ntctcaccac cactttctca 120
cacctagcaa tagtagaatt cagtcctact tctgaggcca gaagaatggt tcagaaaaat 180
antggattat aaaaaataac aattaagaaa aataatc          217
```

<210> 416

<211> 213

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
<222> (1)...(213)
<223> n = A,T,C or G

<400> 416
atgcataatnt aaagganact gcctcgcttt tagaagacat ctggngctgct ctctgcatga 60
ggcacagcag taaagctctt tgattcccag aatcaagaac tctccccttc agactattac 120
cgaatgcaag gtggttaatt gaaggccact aattgatgct caaatagaag gatattgact 180
atattggaac agatggagtc tctactacaa aag 213

<210> 417
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(303)
<223> n = A,T,C or G

<400> 417
nagtcttcag gcccatcagg gaagttcaca ctggagagaa gtcatacata tgtactgtat 60
gtgggaaagg ctttactctg agttcaaadc ttcaagccca tcagagagtc cacactggag 120
agaagccata caaatgcaat gagtgtggga agagcttcag gagggattcc cattatcaag 180
ttcatctagt ggtccacaca ggagagaaac cctataaatg tgagatatgt gggaagggct 240
tcantcaaag ttcgtatctt caaatccatc ngaaggncca cagtatanan aaacctttta 300
agt 303

<210> 418
<211> 328
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(328)
<223> n = A,T,C or G

<400> 418
tttttgccg tggtggggca gggacgggac angagtctca ctctgttgcc caggctggag 60
tgcaacaggca tgatctcggc tcactacaac ccctgcctcc catgtccaag cgattcttgt 120
gcctcagcct tcctgtagc tagaattaca ggcacatgcc accacaacca gctagttttt 180
gtatttttag tagagacagg gtttcacat gttggccagg ctggtctcaa actcctnacc 240
tcagnggtca ggctgggtct aaactcctga cctcaagtga tctgcccacc tcagcctccc 300
aaagtgtan gattacaggc cgtgagcc 328

<210> 419
<211> 389
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(389)
<223> n = A,T,C or G

<400> 419
cctcctcaag acggcctgtg gtccgcctcc cggcaaccaa gaagcctgca gtgccatag 60


```
acccttgagc catggactgg agcctgaaag gcagcgtaca ccctgctcct gatcttgctg 120
cttgtttcct ctctgtggct ccattcatag cacagttggt gcactgaggc ttgtgcaggc 180
cgagcaaggc caagctggct caaagagcaa ccagtcaact ctgccacggg gtgccaggca 240
ccggttctcc agccaaccaac ctcaactcgt cccgcaaata gcacatcagt tctttctacc 300
taaaggtagg accaaagggc atctgctttt ctgaagtcct ctgctctatc agccatcacg 360
tggcagccac tcnggctgtg tcgacgcgg 389
```

<210> 420

<211> 408

<212> DNA

<213> Homo sapiens

<400> 420

```
gttcctccta actcctgcc aaaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaccgaa 180
gtccattga cacttttccc actgacccca taaaggaatc ctcattggca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg aagtgcctatg aaaaacctgg caagccc 408
```

<210> 421

<211> 352

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(352)

<223> n = A,T,C or G

<400> 421

```
gtcaaaaaat ctttttactg atnggcattg ctacacaatc attgactatt acggaggcca 60
gaggagaatg aggcctggcc tgggagccct gtgcctacta naagcacatt agattatcca 120
ttcactgaca gaacaggctt tttttgggtc cttcttctcc accacnata acttgacgtc 180
ctccttcttg aagattcttt ggcagttgtc tttgtcataa cccacagggt tagaaacaag 240
ggtgcaacat gaaatttctg tttcgtagca agtgcatgtc tcacaagttg gcangtctgc 300
cactccgagt ttattgggtg tttgtttcct ttgagatcca tgcatttcct gg 352
```

<210> 422

<211> 337

<212> DNA

<213> Homo sapiens

<400> 422

```
atgccaccat gctggcaatg cagcgggcgg tcgaaggcct gcatatccag cccaagctgg 60
cgatgatcga cggcaaccgt tgcccgaagt tgccgatgcc agccgaagcg gtggtcaagg 120
gcgatagcaa ggtgcccggc atcgcggcgg cgtcaatcct ggccaaggct agccgtgatc 180
gtgaaatggc agctgtcgaa ttgatctacc cgggttatgg catcggcggg cataagggt 240
atccgacacc ggtgcacctg gaagccttgc agcggctggg gccgacgccg attcaccgac 300
gcttcttccg ccggtacggc tggcctatga aaattat 337
```

<210> 423

<211> 310

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
<222> (1)...(310)
<223> n = A,T,C or G

<400> 423
gctcaaaaat ctttttactg atatggcatg gctacacaat cattgactat tagaggccag 60
aggagaatga ggctggcctt gggagccctg tgctactan aagcncatta gattatccat 120
tactgacag aacaggtctt ttttgggtcc ttcttctcca ccacgatata cttgcagtcc 180
tccttcttga agattctttg gcagttgtct ttgtcataac ccacaggtgt anaaacaagg 240
gtgcaacatg aaatttctgt ttcgtagcaa gtgcatgtct cacagttgtc aagtctgccc 300
tccgagttta 310

<210> 424
<211> 370
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(370)
<223> n = A,T,C or G

<400> 424
gctcaaaaat ctttttactg ataggcatgg ctacacaatc attgactatt agaggccaga 60
ggagaatgag gcctggcctg ggagccctgt gcctactaga agcacattag attatccatt 120
cactgacaga acaggtcttt tttgggtcct tcttctccac cacgatatac ttgcagtcct 180
ccttcttgaa gattcttttg cagttgtctt tgtcataacc cacaggtgta gaaacatcct 240
ggttgaatct cctggaactc cctcattagg tatgaaatag catgatgcat tgcataaagt 300
cacgaagggtg gcaaagatca caacgctgcc cagganaaca ttcattgtga taagcaggac 360
tccgtcgacg 370

<210> 425
<211> 216
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(216)
<223> n = A,T,C or G

<400> 425
aattgctatn ntttattttg ccactcaaaa taattaccaa aaaaaaaaaa tnttaaatga 60
taacaacnca acatcaaggn aananaaca ggaatggntg actntgcata aatnggccga 120
anattatcca ttaatntaag gggtgacttc aggnacagc acacagacaa acatgcccag 180
gaggntntca ggaccgctcg atgtntntg aggagg 216

<210> 426
<211> 596
<212> DNA
<213> Homo sapiens

<400> 426
cttccagtga ggataaccct gttgccccgg gccgaggttc tccattaggc tctgattgat 60
tggcagtcag tgatggaagg gtgttctgat cattccgact gcccgaaggg tcgctggcca 120
gctctctgtt ttgctgagtt ggcagtagga cctaatttgt taattaagag tagatgggtga 180
gctgtccttg tattttgatt aacctaatgg ccttcccagc acgactcgga ttcagctgga 240
gacatcacgg caacttttaa tgaaatgatt tgaagggccca ttaaggaggca cttcccgtta 300

```

ttaggcagtt catctgcact gataacttct tggcagctga gctggtcgga gctgtggccc 360
aaacgcacac ttggcttttg gttttgagat acaactctta atcttttagt catgcttgag 420
ggtggatggc cttttcagct ttaacccaat ttgcactgcc ttggaagtgt agccaggaga 480
atacactcat atactcgtgg gcttagaggg cacagcagat gtcattgggc tactgcctga 540
gtcccgtggt tcccatccca ggaccttcca tcggcgagta cctgggagcc cgtgct 596

```

<210> 427

<211> 107

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(107)

<223> n = A,T,C or G

<400> 427

```

gaagaattca agttaggttt attcaaaggg cttacngaga atcctanacc caggncaccag 60
cccgggagca gccttanaga gctcctgttt gactgcccgg ctcagng 107

```

<210> 428

<211> 38

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(38)

<223> n = A,T,C or G

<400> 428

```

gaacttcena anaangactt tattcactat tttacatt 38

```

<210> 429

<211> 544

<212> DNA

<213> Homo sapiens

<400> 429

```

ctttgctgga cggaataaaa gtggacgcaa gcatgacctc ctgatgaggg cgctgcattt 60
attgaagagc ggctgcagcc ctgcggttca gattaaaatc cgagaattgt atagacgccg 120
atatccacga actcttgaag gactttctga tttatccaca atcaaatcat cggttttcag 180
tttggatggt ggctcatcac ctgtagaacc tgacttggcc gtggctggaa tccactcgtt 240
gccttcact tcagttacac ctcaactcacc atcctctcct gttggttctg tgctgcttca 300
agatactaag cccacatttg agatgcagca gccatctccc ccaattcctc ctgtccatcc 360
tgatgtgcag ttaaaaaatc tgccctttta tgatgtcctt gatgttctca tcaagcccac 420
gagtttagtt caaagcagta ttcagcgatt tcaagagaag ttttttattt ttgctttgac 480
acctcaacaa gttagagaga tatgcatatc cagggatttt ttgccagggtg gtaggagaga 540
ttat 544

```

<210> 430

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(507)

<223> n = A,T,C or G

<400> 430

```

cttatcncaa tggggctccc aaacttggt gtgcagtgga aactccgggg gaattttgaa 60
gaacactgac acccatcttc caccgcgaca ctctgattta attgggctgc agtgagaaca 120
gagcatcaat ttaaaaaagct gccagaaatg ttntcctggg cagcgttgtg atctttgccn 180
ccttcgtgac tttatgcaat gcatcatgct atttcatacc taatgaggga gttccaggag 240
attcaaccag gatgtttcta cncctgtggg ttatgacaaa gacaactgcc aaagaatntt 300
caagaaggag gactgcaagt atatcgtggt ggagaagaag gacccaaaaa agacctgttc 360
tgtcagtgaa tggataatct aatgtgcttc tagtaggcac agggctccca ggccaggcct 420
cattctcttc tggcctctaa tagtcaatga ttgtgtagcc atgcctatca gtaaaaagat 480
ttttgagcaa aaaaaaaaaa aaaaaaa

```

507

<210> 431

<211> 392

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(392)

<223> n = A,T,C or G

<400> 431

```

gaaaattcag aatggataaa aacaaatgaa gtacaaaata tttcagattt acatagcgat 60
aaacaagaaa gcacttatca ggaggactta caaatggaag tacactctan aaccatcatc 120
tatcatggct aaatgtgaga ttagcacagc tgtattattt gtacattgca aacacctaga 180
aagagatggg aaacaaaatc ccaggagttt tgtgtgtgga gtcctgggtt ttccaacaga 240
catcattcca gcattctgag attagggnga ttggggatca ttctggagtt ggaatgttca 300
acaaaagtga tgttgttagg taaaatgtac aacttctgga tctatgcaga cattgaaggc 360
gcaatgagtc tggcttttac tctgctgttt ct

```

392

<210> 432

<211> 387

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(387)

<223> n = A,T,C or G

<400> 432

```

ggtatccnta cataatcaaa tatagctgta gtacatgttt tcattggngt agattaccac 60
aaatgcaagg caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg 120
ngtagtccaa gctctcgga gtccagccac tgnгааacat gtcctcttta gattaacctc 180
gtggaacnctn ttgttgnatt gtctgaactg tagngccctg tattttgctt ctgtctgnga 240
attctgttgc ttctggggca tttccttgng atgcagagga ccaccacaca gatgacagca 300
atctgaattg ntccaatcac agctgcgatt aagacatact gaaatcgtag aggaccggga 360
acaacgtata gaacactgga gtccttt

```

387

<210> 433

<211> 281

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(281)

<223> n = A,T,C or G

<400> 433

```
ttcaactagc anagaanact gcttcagggn gtgtaaaatg aaaggcttcc acgcagttat 60
ctgattaaag aacactaaga gagggacaag gctagaagcc gcaggatgtc tacactatag 120
caggcnctat ttgggttggc tggaggagct gtggaaaaca tggagagatt ggcgctggag 180
atcgccgtgg ctattcctcn ttgntattac accagnagg ntctctgtnt gccactgggt 240
tnnaaaaccg ntatacaata atgatagaat aggacacaca t 281
```

<210> 434

<211> 484

<212> DNA

<213> Homo sapiens

<400> 434

```
ttttaaaata agcatttagt gctcagtecc tactgagtag tctttctctc cctcctctctg 60
aattttaattc ttccaacttg caatttgcaa ggattacaca ttccactgtg atgtatattg 120
tgttgcaaaa aaaaaaaagt gtctttgttt aaaattactt ggtttgtgaa tccatcttgc 180
tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa acatctgaag 240
agctagtcta tcagcatctg acagggtgaat tggatgggtc tcagaaccat ttcaccaga 300
cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca taacaaaccc 360
tgctccaatc tgtcacataa aagtctgtga cttgaagttt agtcagcacc cccaccaaac 420
tttatTTTTt tatgtgtttt ttgcaacata tgagtgtttt gaaaataaag taccatgtc 480
ttaa 484
```

<210> 435

<211> 424

<212> DNA

<213> Homo sapiens

<400> 435

```
gcgcgctca gaggcaggtca ctttctgcct tccaagtcct ccttcaagga agccccatgt 60
gggtagcttt caatatcgca ggttcttact cctctgcctc tataagctca aaccaccaa 120
cgatcgggca agtaaaccce ctccctcgcc gacttcggaa ctggcgagag ttcagcgag 180
atgggcctgt ggggaggggg caagatagat gagggggagc ggcatgggtc ggggtgaccc 240
cttgagagaga ggaaaaaggc cacaagaggg gctgccaccg ccactaacgg agatggccct 300
ggtagagacc tttgggggtc tggaacctct ggactcccca tgetctaact cccacactct 360
gctatcagaa acttaaactt gaggattttc tctgtttttc actcgcaata aattcagagc 420
aaac 424
```

<210> 436

<211> 667

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(667)

<223> n = A,T,C or G

<400> 436

```
accttgggaa nactctcaca atataaaggg tcgtagactt tactccaaat tccaaaaagg 60
tcctggccat gtaatcctga aagttttccc aaggtagcta taaaatcctt ataaggggtc 120
agcctcttct ggaattcctc tgatttcaaa gtctactct caagttcttg aaaacgaggg 180
cagttcctga aaggcaggta tagcaactga tcttcagaaa gaggaactgt gtgcaccggg 240
atgggctgcc agagtaggat aggattccag atgctgacac cttctggggg aaacaggggt 300
gccaggtttg tcatagcact catcaaagtc cgggtcaacgt ctgtgcttcg aatataaacc 360
```

```

tgttcatgtt tataggactc attcaagaat tttctatatc tttttcttat atactctcca 420
agttcataat gctgctccat gccagctgg gtgagttggc caaatccttg tggccatgag 480
gattccttta tggggtcagt gggaaagggtg tcaatgggac ttcgggtctcc atgccgaaac 540
accaaagtca caaacttcaa ctcttgggt agtacacttc ggtctagcca gaaaaaaagc 600
agaaacaaga agccaaggct aaggcttgct gccctgccag gaggaggggt gcagctctca 660
tgttgag                                     667

```

<210> 437

<211> 693

<212> DNA

<213> Homo sapiens

<400> 437

```

ctacgtctca accctcattt ttaggtaagg aatcttaagt ccaaagatat taagtgactc 60
acacagccag gtaaggaaag ctggattggc acactaggac tctaccatac cggtttttgt 120
taaagctcag gttaggaggc tgataagctt ggaaggaaact tcagacagct ttttcagatc 180
ataaaagata attcttagcc catgttcttc tccagagcag acctgaaatg acagcacagc 240
aggtactcct ctattttcac ccctcttgct tctactctct gccagtcaga cctgtgggag 300
gccatgggag aaagcagctc tctggatgtt tgtacagatc atggactatt ctctgtggac 360
catttctcca ggttacccta ggtgtcacta ttgggggggac agccagcatc tttagctttc 420
atttgagttt ctgtctgtct tcagtagagg aaacttttgc tcttcacact tcacatctga 480
acacctaact gctgttgctc ctgaggtggg gaaagacaga tatagagctt acagtattta 540
tcctatttct aggcactgag ggctgtgggg taccttgttg tgccaaaaca gatcctgttt 600
taaggacatg ttgcttcaga gatgtctgta actatctggg ggctctgttg gctctttacc 660
ctgcatcatg tgctctcttg gctgaaaatg acc                                     693

```

<210> 438

<211> 360

<212> DNA

<213> Homo sapiens

<400> 438

```

ctgcttatca caatgaatgt tctctggggc agcgttgtga tctttgccac ctctgtgact 60
ttatgcaatg catcatgcta tttcatacct aatgaggagg ttccaggaga ttcaaccagg 120
atgtttctac acctgtgggt tatgacaaag acaactgcc aagaatcttc aagaaggagg 180
actgcaagta tatctggttg agaagaagga cccaaaaaag acctgttctg tcagtgaatg 240
gataatctaa tgtgcttcta gtaggcacag ggctcccagg ccaggcctca ttctcctctg 300
gcctctaata gtcaataatt gtgtagccat gcctatcagt aaaaagattt ttgagcaaac 360

```

<210> 439

<211> 431

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(431)

<223> n = A,T,C or G

<400> 439

```

gttcctnnta actcctgcc aaaaacagctc tctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gcttttttct tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggg gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaaat ctcattggcca caaggatttg 240
gccaaactcac ccagctggggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtccata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgctga cgcggccgcg 420
aatttagtag t                                     431

```

<210> 440
<211> 523
<212> DNA
<213> Homo sapiens

<400> 440
agagataaaag cttagggtcaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaatgtc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240
cttctctcaa ggagaggcaa agaaaggaga tacagtggag acatctggaa agttttctcc 300
actggaaaac tgctactatc tgtttttata tttctgttaa aatatatgag gctacagaac 360
taaaaatttaa aacctctttg tgtcccttgg tcctggaaca tttatgttcc ttttaaagaa 420
acaaaaatca aactttacag aaagatttga tgtatgtaac acatatagca gctcttgaag 480
tatatatatc atagcaaata agtcatctga tgagaacaag cta 523

<210> 441
<211> 430
<212> DNA
<213> Homo sapiens

<400> 441
gttcctccta actcctgcc aaaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggtt tcttggttct gcttttttcc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtccata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420
aatttagtag 430

<210> 442
<211> 362
<212> DNA
<213> Homo sapiens

<400> 442
ctaaggaatt agtagtgttc ccatcacttg tttggagtgt gctattctaa aagattttga 60
tttcttgaaa tgacaattat attttaactt tgggtgggga aagagttata ggaccacagt 120
cttcacttct gatacttgta aattaatctt ttattgcact tgttttgacc attaagctat 180
atgttttagaa atggtcattt tacggaaaaa ttagaaaaat tctgataata gtgcagaata 240
aatgaattaa tgttttactt aatttatatt gaactgtcaa tgacaaataa aaattctttt 300
tgattatatt ttgttttcat ttaccagaat aaaaactaag aattaaaagt ttgattacag 360
tc 362

<210> 443
<211> 624
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1) ... (624)
<223> n = A,T,C or G

<400> 443
ttttttttttt gcaacacaat atacatcaca gtgaaatgtg taatccttgc aaattgcaag 60

```
ttgaaagaat taaattcaga ggaggggaga gaaagagtag tcagtaggga ctgagcacta 120
aatgcttatt ttaaagaaa tgtaaagagc agaaagcaat tcaggctacc ctgccttttg 180
tgctggctag tactccggtc ggtgtcagca gcacgtggca ttgaacattg caatgtggag 240
cccaaaccac agaaaatggg gtgaaattgg ccaactttct attaacttgg cttcctgttt 300
tataaaatat tgtgaataat atcacctact tcaaagggca gttatgaggc ttaaataaac 360
taacgcctac aaaacactta aacatagata acataggtgc aagtactatg tatctggtag 420
atggtaaaca tccttattat taaagtcaac gctaaaatga atgtgtgtgc atatgctaata 480
agtacagaga gagggcactt aaaccaacta agggcctgga gggaagggtt cctggaaaaga 540
ngatgcttgt gctgggtcca aatcttggtc tactatgacc ttggccaaat tatttaaact 600
ttgtccctat ctgctaaaca gatac 624
```

<210> 444

<211> 425

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(425)

<223> n = A,T,C or G

<400> 444

```
gcacatcatt nntcttgcatt tctttgagaa taagaagatc agtaaatagt tcagaagtgg 60
gaagctttgt ccaggcctgt gtgtgaaccc aatgttttgc ttagaaatag aacaagtaag 120
ttcattgcta tagcataaca caaaatttgc ataagtgttg gtcagcaaat ccttgaatgc 180
tgcttaatgt gagagggttg taaaatcctt tgtgcaacac tctaactccc tgaatgtttt 240
gctgtgctgg gacctgtgca tgccagacaa ggccaagctg gctgaaagag caaccagcca 300
cctctgcaat ctgccacctc ctgctggcag gatttgtttt tgcacacctg gaagagccaa 360
ggaggcacca gggcataagt gagtagactt atggtcgacg cggccgcgaa tttagtagta 420
gtaga 425
```

<210> 445

<211> 414

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(414)

<223> n = A,T,C or G

<400> 445

```
catgtttatg nttttggatt actttgggca cctagtgttt ctaaactcgtc tatcattctt 60
ttctgttttt caaaagcaga gatggccaga gtctcaacaa actgtatctt caagtctttg 120
tgaaattctt tgcatgtggc agattatttg atgtagtctt ctttaactag catataaatc 180
tggtgtgttt cagataaatg aacagcaaaa tgtggtggaa ttaccatttg gaacattgtg 240
aatgaaaaat tgtgtctcta gattatgtaa caaataacta tttcctaacc attgatcttt 300
ggatttttat aatcctactc acaaatgact aggtctctcc tcttgtatct tgaagcagtg 360
tggtgtctgg attgataaaa aaaaaaaaaa tgcacgcggc cgcgaattta gtag 414
```

<210> 446

<211> 631

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(631)

<223> n = A,T,C or G

<400> 446

```

acaaattaga anaaagtgcc agagaacacc acataccttg tccggaacat tacaatggct 60
tctgcatgca tgggaagtgt gagcattcta tcaatatgca ggagccatct tgcaggtgtg 120
atgctgggta tactggacaa cactgtgaaa aaaaggacta cagtgttcta tacgttggtc 180
ccggtcctgt acgatttcag tatgtcttaa tcgcagctgt gattggaaca attcagattg 240
ctgtcatctg tgtgggtggtc ctctgcatca caagggccaa actttaggta atagcattgg 300
actgagattt gtaaaccttc caaccttcca ggaaatgcc cagaagcaac agaattcaca 360
gacagaagca aaatacaggg cactacagtt cagacaatac aacaagagcg tccacgaggt 420
taatctaaag ggagcatgtt tcacagtggc tggactaccg agagcttga ctacacaata 480
cagtattata gacaaaagaa taagacaaga gatctacaca tgttgccctg catttgtggt 540
aatctacacc aatgaaaaca tgtactacag ctatatattga ttatgtatgg atatatttga 600
aatagtatac attgtcttga tgttttttct g 631

```

<210> 447

<211> 585

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(585)

<223> n = A,T,C or G

<400> 447

```

ccttgggaaa antntcacia tataaagggt cgtagacttt actccaaatt ccaaaaagggt 60
cctggccatg taatcctgaa agttttccca aggtagctat aaaatcctta taagggtgca 120
gcctcttctg gaattcctct gatttcaaag tctcactctc aagttcttga aaacgagggc 180
agttcctgaa aggcaggtat agcaactgat cttcagaaaag aggaactgtg tgcaccggga 240
tggtctgcca gagtaggata ggattccaga tgctgacacc ttctggggga aacagggctg 300
ccagggttgt catagcactc atcaaagtcc ggtcaacgtc tgtgcttcga atataaacct 360
gttcatgttt ataggactca ttcaagaatt ttctatatct ctttcttata tactctccaa 420
gttcataatg ctgctccatg cccagctggg tgagttggcc aaatccttgt ggccatgagg 480
attcctttat ggggtcagtg ggaaagggtg caatgggact tcggtctcca tgccgaaaca 540
ccaaagtcac aaacttcaac tccttggtca gtacacttcg gtcta 585

```

<210> 448

<211> 93

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(93)

<223> n = A,T,C or G

<400> 448

```

tgctcgtggg tcattctgan nnccgaactg accntgccag ccctgccgan gggecnccat 60
ggctccctag tgccctggag agganggggc tag 93

```

<210> 449

<211> 706

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (706)

<223> n = A,T,C or G

<400> 449

```
ccaagttcat gctntgtgct ggacgctgga caggggggcaa aagcnnttgc tcgtgggtca 60
ttctgancac cgaactgacc atgccagccc tgccgatggt cctccatggc tccctagtgc 120
cctggagagg aggtgtctag tcagagagta gtccctggaag gtggcctctg ngaggagcca 180
cggggacagc atcctgcaga tggtcgggcg cgtcccatc gccattcagg ctgcgcaact 240
gttgggaagg gcgatcggtg cgggcctctt cgctattacg ccagctggcg aaagggggat 300
gtgctgcaag gcgattaagt tgggtaacgc caggggtttc ccagtcncga cgttgtaaaa 360
cgacggccag tgaattgaat ttaggtgacn ctatagaaga gctatgacgt cgcattgcacg 420
cgtacgtaag cttggatcct ctagagcggc cgcctactac tactaaattc gcggccgcgt 480
cgacgtggga tccnactga gagagtggag agtgacatgt gctggacnct gtccatgaag 540
cactgagcag aagctggagg cacaacgcnc cagacactca cagctactca ggaggctgag 600
aacaggttga acctgggagg tggaggttgc aatgagctga gatcaggccn ctgcncccca 660
gcatggatga cagagtgaaa ctccatctta aaaaaaaaaa aaaaaa 706
```

<210> 450

<211> 493

<212> DNA

<213> Homo sapiens

<400> 450

```
gagacggagt gtcactctgt tgcccaggct ggagtgcagc aagacactgt ctaagaaaaa 60
acagttttaa aaggtaaaaa aacataaaaa gaaatatcct atagtggaaa taagagagtc 120
aaatgaggct gagaacttta caaagggatc ttacagacat gtcgccaata tcaactgcatg 180
agcctaagta taagaacaac ctttggggag aaaccatcat ttgacagtga ygtacaattc 240
caagtcagggt agtgaatatg gtggaattaa actcaaatta atcctgccag ctgaaacgca 300
agagacactg tcagagagtt aaaaagttag ttctatccat gaggtgattc cacagtcttc 360
tcaagtcaac acatctgtga actcacagac caagttctta aaccactgtt caaactctgc 420
tacacatcag aatcacctgg agagctttac aaactcccat tgccgagggt cgacgcggcc 480
gcgaatttag tag 493
```

<210> 451

<211> 501

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (501)

<223> n = A,T,C or G

<400> 451

```
gggcgcgtcc cattcgccat tcaggetgcg caactgttgg gaagggcgat cgggtcgggc 60
ctcttcgcta ttacgccagc tggcgaaagg gggatgtgct gcaaggcgat taagttgggt 120
aacgccaggg ttttcccagt cncgacgttg taaaacgacg gccagtgaat tgaatttagg 180
tgacnctata gaagagctat gacgtcgcat gcacgcgtac gtaagcttgg atcctctaga 240
gcggccgcct actactacta aattcgcggc cgcgtcgacg tgggatccnc actgagagag 300
tgagagagtga catgtgctgg acnctgtcca tgaagcactg agcagaagct ggaggcacia 360
cgcncacagc actcacagct actcaggagg ctgagaacag gttgaacctg ggaggtggag 420
gttgcaatga gctgagatca ggcnctgcn cccagcatg gatgacagag tgaaactcca 480
tcttaaaaaa aaaaaaaaaa a 501
```

<210> 452

<211> 51

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)... (51)
<223> n = A,T,C or G

<400> 452
agacgggtttc accntttacaa cnccttttag gatgggnntt ggggagcaag c 51

<210> 453
<211> 317
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)... (317)
<223> n = A,T,C or G

<400> 453
tacatcttgc tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa 60
acatctgaag agctagtcta tcagcatctg gcaagtgaat tggatgggtc tcagaacct 120
ttcacccana cagcctgttt ctatctgtt taataaatta gtttgggtc tctacatgca 180
taacaaaccc tgctccaatc tgtcacataa aagtctgtga cttgaagttt antcagcacc 240
cccaccaaac tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataagg 300
taccatgtc tttatta 317

<210> 454
<211> 231
<212> DNA
<213> Homo sapiens

<400> 454
ttcgaggtag aatcaactct cagagtgtag tttccttcta tagatgagtc agcattaata 60
taagccacgc cacgctcttg aaggagtctt gaattctcct ctgctcactc agtagaacca 120
agaagaccaa attcttctgc atcccagctt gcaaacaaaa ttgttcttct aggtctccac 180
ccttctttt tcagtgttcc aaagctctc acaatttcat gaacaacagc t 231

<210> 455
<211> 231
<212> DNA
<213> Homo sapiens

<400> 455
taccaaagag ggcataataa tcagtctcac agtaggggtc accatcctcc aagtgaaaaa 60
cattgttccg aatgggtttt ccacaggcta cacacacaaa acaggaaaca tgccaagttt 120
gtttcaacgc attgatgact tctccaagga tcttctttg gcatcgacca cattcagggg 180
caaagaattt ctcatagcac agtcacaat acagggtcc tttctctct a 231

<210> 456
<211> 231
<212> DNA
<213> Homo sapiens

<400> 456
ttggcaggta cccttacaaa gaagacacca taccttatgc gttattaggt ggaataatca 60
ttccattcag tattatcgtt attattcttg gagaaacct gtctgtttac tgtaaccttt 120
tgactcaaa ttcctttatc aggaataact acatagccac tatttacaaa gccattggaa 180

cctttttatt tgggtgcagct gctagtcagt ccctgactga cattgccaaag t 231

<210> 457

<211> 231

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(231)

<223> n = A,T,C or G

<400> 457

cgagggtaccc aggggtctga aaatctctnn ttantagtc gatagcaaaa ttgttcatca 60
gcattcctta atatgatctt gctataatta gatttttctc cattagagtt catacagttt 120
tatttgattt tattagcaat ctctttcaga agacccttga gatcattaag ctttgtatcc 180
agttgtctaa atcgatgcct catttcctct gaggtgtcgc tggcttttgt g 231

<210> 458

<211> 231

<212> DNA

<213> Homo sapiens

<400> 458

aggtctggtt cccccactt ccactcccct ctactctctc taggactggg ctgggccaaag 60
agaagagggg tggttaggga agccgttgag acctgaagcc ccaccctcta ccttccttca 120
acaccctaac cttgggtaac agcatttgga attatcattt gggatgagta gaatttccaa 180
ggtcctgggt taggcatttt ggggggccag accccaggag aagaagattc t 231

<210> 459

<211> 231

<212> DNA

<213> Homo sapiens

<400> 459

ggtaccgagg ctgctgaca cagagaaacc ccaacgcgag gaaaggaatg gccagccaca 60
ccttcgcgaa acctgtggtg gccaccagt cctaacggga caggacagag agacagagca 120
gcctgcact gttttccctc caccacagcc atcctgtccc tcattggctc tgtgctttcc 180
actatacaca gtcaccgtcc caatgagaaa caagaaggag caccctccac a 231

<210> 460

<211> 231

<212> DNA

<213> Homo sapiens

<400> 460

gcaggtataa catgctgcaa caacagatgt gactaggaac ggccggtgac atggggaggg 60
cctatcaccc tattcttggg ggctgcttct tcacagtgat catgaagcct agcagcaaat 120
cccacctccc cacacgcaca cggccagcct ggagcccaca gaagggtcct cctgcagcca 180
gtggagcttg gtccagcctc cagtccaccc ctaccaggct taaggataga a 231

<210> 461

<211> 231

<212> DNA

<213> Homo sapiens

<400> 461

cgaggtttga gaagctctaa tgtgcagggg agccgagaag caggcggcct agggaggggc 60

```
gcgtgtgctc cagaagagtg tgtgcatgcc agaggggaaa caggcgcttg tgtgtcctgg 120
gtgggggttca gtgaggagtg ggaaatttgt tcagcagaac caagccgttg ggtgaataag 180
agggggattc catggcactg atagagccct atagtttcag agctgggaat t 231
```

<210> 462

<211> 231

<212> DNA

<213> Homo sapiens

<400> 462

```
aggtaccctc attgtagcca tgggaaaatt gatgttcagt ggggatcagt gaattaaatg 60
gggtcatgca agtataaaaa ttaaaaaaaaa aagacttcat gcccaatctc atatgatgtg 120
gaagaactgt tagagagacc aacagggtag tgggttagag atttccagag ttttacattt 180
tctagaggag gtatttaatt tcttctcact catccagtgt tgtatttagg a 231
```

<210> 463

<211> 231

<212> DNA

<213> Homo sapiens

<400> 463

```
tactccagcc tgggtgacaga gcgagaccct atcaccgccc cccacccac caaaaaaaaa 60
actgagtaga cagggtgcct cttggcatgg taagtcttaa gtcccctccc agatctgtga 120
catttgacag gtgtcttttc ctctggacct cgggtgtccc atctgagtga gaaaaggcag 180
tggggagggtg gatcttccag tcgaagcggc atagaagccc gtgtgaaaag c 231
```

<210> 464

<211> 231

<212> DNA

<213> Homo sapiens

<400> 464

```
gtactctaag attttatcta agttgccttt tctgggtggg aaagtttaac cttagtgtact 60
aaggacatca catatgaaga atgtttaagt tggagggtggc aacgtgaatt gcaaacaggg 120
cctgcttcag tgactgtgtg cctgtagtcc cagctactcg ggagtctgtg tgaggccagg 180
gggtgccagcg caccagctag atgctctgta acttctagtc cccattttcc c 231
```

<210> 465

<211> 231

<212> DNA

<213> Homo sapiens

<400> 465

```
catgttggtg tagctgtggt aatgctggct gcattctcaga cagggttaac ttcagctcct 60
gtggcaaatt agcaacaaat tctgacatca tatttatggg ttctgtatct ttgttgatga 120
aggatggcac aatttttgct tgtgttcata atatactcag attagttcag ctccatcaga 180
taaactggag acatgcagga cattagggta gtgtttagc tctggtaatg a 231
```

<210> 466

<211> 231

<212> DNA

<213> Homo sapiens

<400> 466

```
caggtaacct tttccattgg atactgtgct agcaagcatg ctctccgggg tttttttaat 60
ggccttcgaa cagaacttgc cacataacca ggtataatag tttctaacat ttgccagga 120
cctgtgcaat caaatattgt ggagaattcc cttagctggag aagtcacaaa gactataggc 180
aataatggag accagtccca caagatgaca accagtcggt gtgtgcggct g 231
```

<210> 467
 <211> 311
 <212> DNA
 <213> Homo sapiens

<400> 467
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<211> 2229

<212> DNA

<213> Homo sapiens

<400> 469

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<210> 470

<211> 2426

<212> DNA

<213> Homo sapiens

<400> 470

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<211> 812

<212> DNA

<213> Homo sapiens

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<211> 515

<212> DNA

<213> Homo sapiens

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<400> 472

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<211> 5829

<212> DNA

<213> Homo sapiens

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<210> 474

<211> 1594

<212> DNA

<213> Homo sapiens

<400> 474

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<210> 475

<211> 2414
 <212> DNA
 <213> Homo sapiens

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 <221> unsure
 <222> (33)
 <223> n=A,T,C or G

<400> 475
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<210> 476
 <211> 3434
 <212> DNA
 <213> Homo sapiens

<400> 476

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			20					25					30		
Leu	Ser	His	Tyr	His	Arg	Asp	Thr	Arg	His	His	Thr	Val	Thr	Trp	Thr
		35					40					45			
His	His	His	Thr	His	Glu	His	Thr	Asp	Thr	Leu	Pro	Tyr	Gly	His	Trp
	50					55					60				
His	Thr	His	Cys	His	Thr	Val	Thr	Trp	Thr	His	Leu	His	Thr	Ile	Thr
65					70					75					80
Pro	Pro	His	Thr	Leu	Pro	Val	Asp	Thr	Arg	Thr	His	Arg	His	Cys	His
				85					90					95	
Thr	Asp	Thr	Gln	Asn	Thr	Val	Thr	Arg	Arg	His	His	His	Ala	Asp	Thr
			100					105					110		
Pro	Pro	Leu	Trp	Cys	Arg	Leu	Asn	Tyr	Pro	Ala	Gly	Gly	Thr	Ala	Val
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<210> 478
<211> 143
<212> PRT
<213> Homo sapiens
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Met	Tyr	Arg	His	Thr	Glu	Thr	Leu	Pro	His	Gly	Asp	Thr	Val	Thr	Gln
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			20					25					30		
Gly	Glu	Ile	Thr	Trp	Thr	His	His	His	Thr	Ile	Thr	Gly	Thr	Gln	Thr
		35					40					45			
His	Gly	Asp	Ile	Thr	Thr	Trp	Thr	His	Cys	His	Thr	Thr	Thr	Gly	Thr
	50					55					60				
Arg	Asp	Ile	Thr	Leu	Ser	His	Gly	His	Thr	Ile	Thr	His	Met	Asn	Thr
65					70					75					80
Pro	Thr	His	Cys	His	Met	Asp	Thr	Gly	Thr	His	Thr	Ala	Thr	Leu	Ser
				85					90					95	

<210> 480

<211> 144

<212> PRT

<213> Homo sapiens

<400> 480

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Met Glu Pro Tyr Arg Gly Asn Glu Gln Pro Ser Gln Glu Gln Gly Val
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Cys Cys Leu Trp Gly Leu Gln Ser Leu Pro Gln Gly Ser Tyr Val Thr
      20                      25                      30

Val Gly Phe Leu Val Val Lys Arg Gln Thr Ile Gly Arg Leu Glu Arg
      35                      40                      45

Asp Phe Met Phe Lys Cys Arg Lys Gln Pro Gly Leu Pro Pro Ser Gly
      50                      55                      60

Leu Cys Leu Leu Trp Pro Trp Pro Asn Leu Glu Phe Gly Arg Arg Gln
      65                      70                      75                      80

Asp Arg Leu Thr Trp Ser Ser Val Ser Val Ala Gly Val Cys Ala Cys
      85                      90                      95

Arg Ala Arg Pro Gly Trp Leu Gly Glu Gln Pro Ala Thr Ser Ala Gly
      100                     105                     110

Val Arg Leu Glu Gln Val Glu Gln Pro Pro Ala His Pro Leu Gln Glu
      115                     120                     125

Ala Gly Val Ala Arg Phe Pro Arg Pro Glu Trp Val Pro Pro Asn Gly
      130                     135                     140

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<210> 481

<211> 167

<212> PRT

<213> Homo sapiens

<400> 481

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Met His Gly Pro Gln Val Leu Ala Arg Cys Ser Glu Cys Ala Cys Pro
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Ala Leu Ala Ala Thr Ser Ala Gly Val Arg Leu Glu Gly Val Asp Arg
      20                      25                      30

Pro Pro Thr Leu Pro Ser Gln Gly Ser Gly Trp Pro Cys Ser His Ser
      35                      40                      45

Leu Ser Gly Cys His Leu Met Ala Asp Gly Ala Lys Ala Leu Gly Lys
      50                      55                      60

Ala Asp Gly Pro Trp Pro Tyr Leu Phe Val Arg Arg Thr Asp Val Pro

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[illegible]

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<210> 482
<211> 143
<212> PRT
<213> Homo sapiens
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<400> 482
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Pro Cys Leu Trp Gly Ser Ser Pro Cys Leu Arg Cys His Met Ala Leu
      20                        25                      30

Arg Ala Ser Trp Leu Pro Gly Gly Gly Pro Gln Ala Ile Leu Gly Arg
      35                        40                      45

Thr Leu Cys Ser Ser Ala Glu Ser Ser Gln Asp Cys His Pro Gly Gly
      50                        55                      60

Pro Ser Ile Ala Leu Ala Lys Pro Cys Arg Gly Val Trp Leu Leu Phe
      65                        70                      75                      80

Glu Pro Ala Trp Pro Pro Trp His Ala Arg Ala Pro Gly Ala Gly Thr
      85                        90                      95

Leu Leu Arg Val Cys Leu Ser Cys Leu Gly Cys His Leu Cys Gly Gly
      100                       105                     110

Ala Ser Gly Gly Gly Gly Pro Ala Thr Asn Leu Thr Gln Ser Arg Lys
      115                       120                     125

Trp Met Ala Met Phe Pro Gln Pro Glu Trp Leu Pro Pro Asp Gly
      130                       135                     140
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<210> 483
<211> 143
<212> PRT
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<213> Homo sapiens

<400> 483

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Cys Cys Leu Trp Gly Ser Ser Pro Cys Leu Gly Ser Tyr Gly Thr Ala
      20              25              30

Gly Phe Leu Val Ala Lys Arg Arg Thr Thr Gly Leu Leu Glu Glu Asp
      35              40              45

Phe Thr Phe Lys Cys Arg Lys Gln Pro Lys Leu Pro Ser Met Arg Leu
      50              55              60

Ser Leu Leu Trp Pro Trp Arg Asp Leu Lys Phe Val Pro Arg Gln Asp
      65              70              75              80

Lys Leu Thr Arg Ser Ser Val Ser Val Ala Gly Ala Tyr Ala Cys Arg
      85              90              95

Ala Gly Pro Gly Trp Leu Lys Glu Gln Pro Ala Thr Ser Ala Arg Val
      100             105             110

Arg Leu Val Gln Ala Glu His Pro Pro Pro His Pro Leu Glu Glu Val
      115             120             125

Gly Met Ala Arg Phe Pro Gln Pro Glu Cys Leu Pro Pro Tyr Cys
      130             135             140

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<210> 484

<211> 30

<212> PRT

<213> Homo Sapien

<400> 484

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Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
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Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile
      20              25              30

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<210> 485

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 485

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<210> 486

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 486

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27

<210> 487

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 487

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36

<210> 488

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 488

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33

<210> 489

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 489

Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala
1 5 10 15
Ser Val Ala

<210> 490

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 490

Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys
1 5 10 15
Leu Ser His Ser
20

<210> 491

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 491

Thr	Cys	Leu	Ser	His	Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu
1				5					10					15	
Thr	Gly	Phe	Thr												
				20											

<210> 492

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 492

Ala	Leu	Thr	Gly	Phe	Thr	Phe	Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr
1				5					10					15	
Leu	Ala	Ser	Leu												
				20											

<210> 493

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 493

Tyr	Thr	Leu	Ala	Ser	Leu	Tyr	His	Arg	Glu	Lys	Gln	Val	Phe	Leu	Pro
1				5					10					15	
Lys	Tyr	Arg	Gly												
				20											

<210> 494

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 494

Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly	Gly	Ala	Ser	Ser	Glu	Asp	Ser
1				5					10					15	
Leu	Met	Ile	Ser												
				20											

<210> 495

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 495

Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro Gly Ala Pro
1 5 10 15
Phe Pro Asn Gly
20

<210> 496

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 496

Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu Leu
1 5 10 15
Pro Pro Pro Pro Ala
20

<210> 497

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 497

Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val
1 5 10 15
Ser Val Arg Val
20

<210> 498

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 498

Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val
1 5 10 15
Val Pro Gly Arg
20

<210> 499

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 499

```
Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 1           5           10           15
Ser Ala Phe Leu
                20
```

<210> 500

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 500

```
Leu Asp Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met
 1           5           10           15
Gly Ser Ile Val
                20
```

<210> 501

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 501

```
Phe Met Gly Ser Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met
 1           5           10           15
Val Ser Ala Ala
                20
```

<210> 502

<211> 414

<212> DNA

<213> Homo Sapien

<220>

<221> misc_feature

<222> (1)...(414)

<223> n = A,T,C or G

<400> 502

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caccatggag acaggcctgc gctggctttt cctggctcgt gtgctcaaag gtgtccaatg      60
tcagtcggtg gaggagtcg ggggtcgccg ggtcacgcct gggacacctt tgacantcac      120
ctgtagagtt tttggaatng acctcagtag caatgcaatg agctgggtcc gccaggctcc      180
agggaagggg ctggaatgga tcggagccat tgataattgt ccacantacg cgacctgggc      240
gaaaggccga ttnatnattn ccaaaacctn gaccacggtg gatttgaaaa tgaccagtcc      300
gacaaccgag gacacggcca cctatttttg tggcagaatg aatactggta atagtggttg      360
gaagaatatt tggggcccag gcaccctggt caccgtntcc tcagggaac ctaa          414
```

<210> 503

<211> 379

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<222> (1)...(379)

<223> n = A,T,C or G

<400> 503

atnccgatggt	gcttgggtcaa	aggtgtccag	tgtagtcgg	tggaggagtc	cggggggtcgc	60
ctgggtcacgc	ctgggacacc	cctgacactc	acctgcaccg	tntctggatt	ngacatcagt	120
agctatggag	tgagctgggt	ccgccaggct	ccagggaagg	ggctgggnata	catcggtatca	180
ttagtagtag	tggtacattt	tacgcgagct	gggcgaaagg	ccgattcacc	atttccaaaa	240
cctngaccac	ggtggatttg	aaaatcacca	gtttgacaac	cgaggacacg	gccacctatt	300
tntgtgccag	aggggggttt	aattataaag	acatttgggg	cccaggcacc	ctgggtcacgc	360
tntccttagg	gcaacctaa					379

<210> 504

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 504

Gly	Phe	Thr	Asn	Tyr	Thr	Asp	Phe	Glu	Asp	Ser	Pro	Tyr	Phe	Lys	Glu
1			5					10					15		
Asn	Ser	Ala													

<210> 505

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 505

Lys	Glu	Asn	Ser	Ala	Phe	Pro	Pro	Phe	Cys	Cys	Asn	Asp	Asn	Val	Thr
1				5				10					15		
Asn	Thr	Ala	Asn												
				20											

<210> 506

<211> 407

<212> DNA

<213> Homo Sapien

<400> 506

atggagacag	gectgcgctg	gcttctcctg	gtcgtgcgc	tcaaaggtgt	ccagtgtcag	60
tcgctggagg	agtcggggg	tcgctgggtc	acgcctggga	cacccctgac	actcacctgc	120
accgtctctg	gattctccct	cagtagcaat	gcaatgatct	gggtccgcca	ggctccaggg	180
aaggggctgg	aatacatcgg	atacattagt	tatggtggta	gcgcatacta	cgcgagctgg	240
gtgaaaggcc	gattcaccat	ctccaaaacc	tcgaccacgg	tggatctgag	aatgaccagt	300
ctgacaaccg	aggacacggc	cacctatttc	tgtgccagaa	atagtgattt	tagtggtatg	360
ttgtggggcc	caggcaccct	ggtcaccgtc	tcctcagggc	aacctaa		407

<210> 507
 <211> 422
 <212> DNA
 <213> Homo Sapien

<400> 507
 atggagacag gcctgcgctg gcttctcctg gtcgctgtgc tcaaagggtg ccagtgtcag 60
 tcggtggagg agtccggggg tcgcctgggc acgcctggga caccctgac actcacctgt 120
 acagtctctg gattctccct cagcaactac gacctgaact gggtcgcca ggctccaggg 180
 aaggggctgg aatggatcgg gatcattaat tatgttggtg ggacggacta cgcgaactgg 240
 gcaaaaggcc gggtcaccat ctccaaaacc tcgaccaccg tggatctcaa gatcgccagt 300
 ccgacaaccg aggacacggc cacctatttc tgtgccagag ggtggaagtg cgatgagtct 360
 ggtccgtgct tgcgcatctg gggcccaggc accctgggtc ccgtctcctt agggcaacct 420
 aa 422

<210> 508
 <211> 411
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> misc_feature
 <222> (1)...(411)
 <223> n = A,T,C or G

<400> 508
 atggagacag gcctcgctgg cttctcctgg tcgctgtgct caaagggtgc cagtgtcagt 60
 cggtaggagga gtccgggggt cgctgggtca cgcctgggac acccctgaca ctcacctgca 120
 cagtctctgg aatcgacctc agtagctact gcatgagctg ggtccgccag gctccaggga 180
 aggggctgga atggatcgga atcattggta ctctgggtga cacatactac gcgagggtggg 240
 cgaaaggccg attcaccatc tccaaaacct cgaccacggg gcatntgaaa atcncagtc 300
 cgacaaccga ggacacggcc acctatttct gtgccagaga tcttcgggat ggtagtagta 360
 ctggttatta taaaatctgg ggcccaggca ccctgggtcac cgtctccttg g 411

<210> 509
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 509
 Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
 1 5 10 15

<210> 510
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 510
 Pro Glu Tyr Asn Arg Pro Leu Leu Ala Asn Asp Leu Met Leu Ile
 1 5 10 15

<210> 511
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 511

Tyr	His	Pro	Ser	Met	Phe	Cys	Ala	Gly	Gly	Gly	Gln	Asp	Gln	Lys
1				5					10					15

<210> 512
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 512

Asp	Ser	Gly	Gly	Pro	Leu	Ile	Cys	Asn	Gly	Tyr	Leu	Gln	Gly	Leu
1				5					10					15

<210> 513
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 513

Ala	Pro	Cys	Gly	Gln	Val	Gly	Val	Pro	Asx	Val	Tyr	Thr	Asn	Leu
1				5					10					15

<210> 514
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 514

Leu	Cys	Lys	Phe	Thr	Glu	Trp	Ile	Glu	Lys	Thr	Val	Gln	Ala	Ser
1				5					10					15

<210> 515
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 515

Met	Val	Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg
1				5				10					15	

<210> 516

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 516

Val	Ser	Glu	Ser	Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln
1				5				10					15	

<210> 517

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 517

Glu	Val	Cys	Ser	Lys	Leu	Tyr	Asp	Pro	Leu	Tyr	His	Pro	Ser	Met
1				5				10					15	

<210> 518

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 518

Arg	Ala	Glu	Pro	Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly
1				5				10					15	

<210> 519

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 519

Arg	Ala	Glu	Pro	Gly	Thr	Glu	Ala	Arg	Arg	Asn	Tyr	Asp	Glu	Gly	Cys
1				5				10					15		

Gly

<210> 520

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 520

Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	Pro	Gly	Thr
1				5				10						15	
Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly							
		20					25								

<210> 521

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 521

Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser	Gly	Leu	Leu
1				5				10						15	
Pro	Pro	Pro	Pro	Ala											
				20											

<210> 522

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 522

Leu	Leu	Val	Val	Pro	Ala	Ile	Lys	Lys	Asp	Tyr	Gly	Ser	Gln	Glu	Asp
1				5					10					15	
Phe	Thr	Gln	Val												
				20											

<210> 523

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<220>

<221> VARIANT

<222> (1)...(254)

<223> Xaa = any amino acid

<400> 523

Met	Ala	Thr	Ala	Gly	Asn	Pro	Trp	Gly	Trp	Phe	Leu	Gly	Tyr	Leu	Ile
1				5				10						15	
Leu	Gly	Val	Ala	Gly	Ser	Leu	Val	Ser	Gly	Ser	Cys	Ser	Gln	Ile	Ile
		20					25				30				
Asn	Gly	Glu	Asp	Cys	Ser	Pro	His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu
		35					40						45		

```

Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln
  50          55          60
Trp Val Leu Ser Ala Thr His Cys Phe Gln Asn Ser Tyr Thr Ile Gly
  65          70          75          80
Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met
          85          90          95
Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu
          100          105          110
Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu
          115          120          125
Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala
          130          135          140
Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg
          145          150          155          160
Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu
          165          170          175
Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys
          180          185          190
Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser Gly
          195          200          205
Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly
          210          215          220
Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu
          225          230          235          240
Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
          245          250

```

<210> 524

<211> 765

<212> DNA

<213> Homo sapien

<400> 524

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atggccacag caggaaatcc ctggggctgg ttctctggggt acctcatcct tgggtgtcgca      60
ggatcgctcg tctctggtag ctgcagccaa atcataaacg gcgaggactg cagccccgcac      120
tcgcagccct ggcaggcggc actggtcatg gaaaacgaat tggtctgctc gggcgctcctg      180
gtgcatccgc agtgggtgct gtcagccgca cactgtttcc agaactccta caccatcggg      240
ctgggctcgc acagtcttga ggccgaccaa gagccaggga gccagatggt ggaggccagc      300
ctctccgtac ggcaccaga gtacaacaga cccttgctcg ctaacgacct catgctcatc      360
aagttggacg aatccgtgtc cgagtctgac accatccgga gcatcagcat tgcttcgcag      420
tgccctaccg cggggaactc ttgctctgtt tctggctggg gtctgctggc gaacggcaga      480
atgcctaccg tgctgcagtg cgtgaacgtg tcggtggtgt ctgaggaggt ctgcagtaag      540
ctctatgacc cgctgtacca ccccagcatg ttctgcgccg gcggagggca agaccagaag      600
gactcctgca acggtgactc tggggggccc ctgatctgca acgggtactt gcagggcctt      660
gtgtctttcg gaaaagcccc gtgtggccaa gttggcgtgc caggtgtcta caccaacctc      720
tgcaaattca ctgagtggat agagaaaacc gtccaggcca gtttaa      765

```

<210> 525

<211> 254

<212> PRT

<213> Homo sapien

<400> 525

```

Met Ala Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile
  1          5          10          15
Leu Gly Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile
          20          25          30
Asn Gly Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu

```

35	40	45
Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln		
50	55	60
Trp Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly		
65	70	75
Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met		
85	90	95
Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu		
100	105	110
Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu		
115	120	125
Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala		
130	135	140
Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg		
145	150	155
Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu		
165	170	175
Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys		
180	185	190
Ala Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly		
195	200	205
Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly		
210	215	220
Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu		
225	230	235
Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser		
245	250	

<210> 526

<211> 963

<212> DNA

<213> Homo sapiens

<400> 526

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atgagttcct gcaacttcac acatgccacc tttgtgctta ttggtatccc aggattagag 60
aaagcccat tctgggttgg cttccccctc ctttccatgt atgtagtggc aatgttttga 120
aactgcatcg tggctcttcat cgtaaggacg gaacgcagcc tgcacgctcc gatgtacctc 180
tttctctgca tgcttgacgc cattgacctg gccttatcca catccaccat gcctaagatc 240
cttgcccttt tctggtttga ttcccgagag attagctttg aggcctgtct taccagatg 300
ttctttatcc atgccccttc agccattgaa tccaccatcc tgctggccat ggcctttgac 360
cgttatgtgg ccatctgcca cccactgcgc catgctgcag tgctcaacaa tacagtaaca 420
gccagattg gcatcgtagc tgtgggtcgc ggatccctct tttttttccc actgcctctg 480
ctgatcaagc ggctggcctt ctgccactcc aatgtcctct cgcactccta ttgtgtccac 540
caggatgtaa tgaagttggc ctatgcagac actttgccc aatgtgtgata tggctctact 600
gccattctgc tggctcatgg cgtaggacgta atgttcatct ccttgctcta tttctgata 660
atacgaacgg ttctgcaact gccttccaag tcagagcggg ccaaggcctt tggaaacctg 720
gtgtcacaca ttggtgtggt actcgccttc tatgtgccac ttattggcct ctcagttgta 780
caccgctttg gaaacagcct tcatccatt gtgcgtgttg tcatgggtga catctacctg 840
ctgctgcctc ctgtcatcaa tcccatcatt tatggtgcca aaaccaaaca gatcagaaca 900
cgggtgctgg ctatgttcaa gatcagctgt gacaaggact tgcaggctgt gggaggcaag 960
tga

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<210> 527

<211> 320

<212> PRT

<213> Homo sapiens

<400> 527

Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile
 5 10 15
 Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
 20 25 30
 Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val
 35 40 45
 Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
 50 55 60
 Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
 65 70 75 80
 Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Phe Glu Ala Cys
 85 90 95
 Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
 100 105 110
 Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
 115 120 125
 Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly
 130 135 140
 Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
 145 150 155 160
 Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
 165 170 175
 Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu
 180 185 190
 Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
 195 200 205
 Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val
 210 215 220
 Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
 225 230 235 240
 Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
 245 250 255
 Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg
 260 265 270
 Val Val Met Gly Asp Ile Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
 275 280 285
 Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
 290 295 300
 Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln Ala Val Gly Gly Lys

305
210 528
211 20
212 DNA
213 Homo Sapien
400 528
actatgggtcc agaggctgtg 20
210 529
211 20
212 DNA
213 Homo Sapien
400 529
atcacctatg tgccgcctct 20
210 530
211 1852
212 DNA
213 Homo sapiens
400 530
ggcacgagaa ttaaaaccct cagcaaaaaca ggcatagaag ggacatacct taaagtaata 60
aaaaccaccc atgacaagcc cacagccaac ataatactaa atggggaaaa gttagaagca 120
tttcctctga gaactgcaac aataaataca aggatgctgg attttgtcaa atgccttttc 180
tgtgtctgtt gagatgctta tgtgactttg cttttaattc tgtttatgtg attatcacat 240
ttattgactt gcctgtgtta gaccggaaga gctgggggtg ttctcaggag ccaccgtgtg 300
ctgcggcagc ttccgggataa cttgaggctg catcactggg gaagaaacac aytccgtgtc 360
gtggcgctga tggctgagga cagagcttca gtgtggcttc tctgcgactg gcttcttcgg 420
ggagtctctc cttcatagtt catccatatt gctccagagg aaaattatat tattttgtta 480
tggatgaaga gtattacgtt gtgcagatat actgcagtgt cttcatctct tgatgtgtga 540
ttgggtaggt tccaccatgt tgccgcagat gacatgattt cagtacctgt gtctggctga 600
aaagtgtttg tttgtgaatg gatattgttg tttctggatc tcatcctctg tgggtggaca 660
gctttctcca ccttgctgga agtgacctgc tgtccagaag tttgatggct gaggagtata 720
ccatcgtgca tgcattcttc atttctctgca tttcttcttc cctggatgga cagggggagc 780
ggcaagagca acgtgggcac ttctggagac cacaacgact cctctgtgaa gacgcttggg 840
agcaagagggt gcaagtgggt ctgccactgc ttcccctgct gcagggggag cggcaagagc 900
aacgtgggtc cttggggaga ctacgatgac agcgccttca tggatcccag gtaccacgtc 960
catggagaag atctggacaa gctccacaga gctgcctggg ggggtaaaagt ccccagaaag 1020
gatctcatcg tcatgctcag ggacacggat gtgaacaaga gggacaagca aaagaggact 1080
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Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr His Val His Gly Glu
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Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Arg Asp
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Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser
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<211> 1228

<212> PRT

<213> Homo sapiens

<400> 537

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Asn Leu Cys Ser Arg Val Phe Phe Trp Trp Leu Asn Pro Leu Phe Lys
          20                      25                      30

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Ile Gly His Lys Arg Arg Leu Glu Glu Asp Asp Met Tyr Ser Val Leu
          35                      40                      45

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Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu Leu Gln Gly Phe Trp
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Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala Gln Lys Pro Ser Leu

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Ile Phe Thr Leu	Ile Glu Glu Ser Ala	Lys Val Ile Gln	Pro Ile Phe			
	100	105	110			
Leu Gly Lys Ile	Ile Asn Tyr Phe	Glu Asn Tyr Asp	Pro Met Asp Ser			
	115	120	125			
Val Ala Leu Asn	Thr Ala Tyr Ala	Tyr Ala Thr	Val Leu Thr	Phe Cys		
	130	135	140			
Thr Leu Ile Leu	Ala Ile Leu His	His Leu Tyr	Phe Tyr His	Val Gln		
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Cys Ala Gly Met	Arg Leu Arg Val	Ala Met Cys	His Met Ile	Tyr Arg		
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Lys Ala Leu Arg	Leu Ser Asn Met	Ala Met Gly	Lys Thr Thr	Thr Gly		
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Gln Ile Val Asn	Leu Leu Ser Asn	Asp Val Asn	Lys Phe Asp	Gln Val		
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Thr Val Phe Leu	His Phe Leu Trp	Ala Gly Pro	Leu Gln Ala	Ile Ala		
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Val Thr Ala Leu	Leu Trp Met Glu	Ile Gly Ile	Ser Cys Leu	Ala Gly		
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Met Ala Val Leu	Ile Ile Leu Leu	Pro Leu Gln	Ser Cys Phe	Gly Lys		
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Ile Arg Thr Met	Asn Glu Val Ile	Thr Gly Ile	Arg Ile Ile	Lys Met		
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Tyr Ala Trp Glu	Lys Ser Phe Ser	Asn Leu Ile	Thr Asn Leu	Arg Lys		
	290	295	300			
Lys Glu Ile Ser	Lys Ile Leu Arg	Ser Ser Cys	Leu Arg Gly	Met Asn		
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	325	330	335			
Thr Thr Tyr Val	Leu Leu Gly Ser	Val Ile Thr	Ala Ser Arg	Val Phe		
	340	345	350			
Val Ala Val Thr	Leu Tyr Gly Ala	Val Arg Leu	Thr Val Thr	Leu Phe		
	355	360	365			
Phe Pro Ser Ala	Ile Glu Arg Val	Ser Glu Ala	Ile Val Ser	Ile Arg		
	370	375	380			

Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg
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 Gln Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr
 405 410 415
 Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser
 420 425 430
 Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val Val Gly Pro Val Gly
 435 440 445
 Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro
 450 455 460
 Ser His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln
 465 470 475 480
 Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly
 485 490 495
 Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala
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 Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile
 515 520 525
 Gly Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln Lys Ala Arg Val Asn
 530 535 540
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 Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu
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 Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His
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 Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp
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 Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu Phe Leu Lys Ser Gly
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 Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn Glu Glu Ser Glu Gln
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 Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu
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 Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly
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 Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu
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Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr
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 Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val Thr Val Asn Gly Gly
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 Gly Asn Val Thr Glu Lys Leu Asp Leu Asn Trp Tyr Leu Gly Ile Tyr
 755 760 765
 Ser Gly Leu Thr Val Ala Thr Val Leu Phe Gly Ile Ala Arg Ser Leu
 770 775 780
 Leu Val Phe Tyr Val Leu Val Asn Ser Ser Gln Thr Leu His Asn Lys
 785 790 795 800
 Met Phe Glu Ser Ile Leu Lys Ala Pro Val Leu Phe Phe Asp Arg Asn
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 Pro Ile Gly Arg Ile Leu Asn Arg Phe Ser Lys Asp Ile Gly His Leu
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 Asp Asp Leu Leu Pro Leu Thr Phe Leu Asp Phe Ile Gln Thr Leu Leu
 835 840 845
 Gln Val Val Gly Val Val Ser Val Ala Val Ala Val Ile Pro Trp Ile
 850 855 860
 Ala Ile Pro Leu Val Pro Leu Gly Ile Ile Phe Ile Phe Leu Arg Arg
 865 870 875 880
 Tyr Phe Leu Glu Thr Ser Arg Asp Val Lys Arg Leu Glu Ser Thr Thr
 885 890 895
 Arg Ser Pro Val Phe Ser His Leu Ser Ser Ser Leu Gln Gly Leu Trp
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 915 920 925
 Ala His Gln Asp Leu His Ser Glu Ala Trp Phe Leu Phe Leu Thr Thr
 930 935 940
 Ser Arg Trp Phe Ala Val Arg Leu Asp Ala Ile Cys Ala Met Phe Val
 945 950 955 960
 Ile Ile Val Ala Phe Gly Ser Leu Ile Leu Ala Lys Thr Leu Asp Ala
 965 970 975
 Gly Gln Val Gly Leu Ala Leu Ser Tyr Ala Leu Thr Leu Met Gly Met
 980 985 990
 Phe Gln Trp Cys Val Arg Gln Ser Ala Glu Val Glu Asn Met Met Ile

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Trp Glu Tyr Gln Lys Arg Pro Pro Pro Ala Trp Pro His Glu Gly Val 1025 1030 1035 1040		
Ile Ile Phe Asp Asn Val Asn Phe Met Tyr Ser Pro Gly Gly Pro Leu 1045 1050 1055		
Val Leu Lys His Leu Thr Ala Leu Ile Lys Ser Gln Glu Lys Val Gly 1060 1065 1070		
Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser Leu Ile Ser Ala Leu 1075 1080 1085		
Phe Arg Leu Ser Glu Pro Glu Gly Lys Ile Trp Ile Asp Lys Ile Leu 1090 1095 1100		
Thr Thr Glu Ile Gly Leu His Asp Leu Arg Lys Lys Met Ser Ile Ile 1105 1110 1115 1120		
Pro Gln Glu Pro Val Leu Phe Thr Gly Thr Met Arg Lys Asn Leu Asp 1125 1130 1135		
Pro Phe Asn Glu His Thr Asp Glu Glu Leu Trp Asn Ala Leu Gln Glu 1140 1145 1150		
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Val Cys Leu Ala Arg Ala Ile Leu Arg Lys Asn Gln Ile Leu Ile Ile 1185 1190 1195 1200		
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 Asp Pro Met Asp Ser Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr
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 Val Leu Thr Phe Cys Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr
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 Phe Tyr His Val Gln Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys
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 His Met Ile Tyr Arg Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly
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 145 150 155 160
 Lys Phe Asp Gln Val Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro
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 Leu Gln Ala Ile Ala Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile
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 Ser Cys Leu Ala Gly Met Ala Val Leu Ile Ile Leu Leu Pro Leu Gln
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705					710					715					
Tyr	Leu	Gly	Ile	Tyr	Ser	Gly	Leu	Thr	Val	Ala	Thr	Val	Leu	Phe	Gly
725					730					735					
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Cys	Ala	Met	Phe	Val	Ile	Ile	Val	Ala	Phe	Gly	Ser	Leu	Ile	Leu	Ala
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Lys	Thr	Leu	Asp	Ala	Gly	Gln	Val	Gly	Leu	Ala	Leu	Ser	Tyr	Ala	Leu
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Glu	Asn	Met	Met	Ile	Ser	Val	Glu	Arg	Val	Ile	Glu	Tyr	Thr	Asp	Leu
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 Arg Lys Asn Leu Asp Pro Phe Asn Glu His Thr Asp Glu Glu Leu Trp
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 Gly Lys Met Asp Thr Glu Leu Ala Glu Ser Gly Ser Asn Phe Ser Val
 1125 1130 1135
 Gly Gln Arg Gln Leu Val Cys Leu Ala Arg Ala Ile Leu Arg Lys Asn
 1140 1145 1150
 Gln Ile Leu Ile Ile Asp Glu Ala Thr Ala Asn Val Asp Pro Arg Thr
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 Asp Glu Leu Ile Gln Lys Lys Ile Arg Glu Lys Phe Ala His Cys Thr
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 Val Leu Thr Ile Ala His Arg Leu Asn Thr Ile Ile Asp Ser Asp Lys
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199

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<213> Homo sapiens

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Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala
5 10 15

Ser Val

<210> 546

<211> 29

<212> PRT

<213> Homo sapiens

<400> 546

Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly
5 10 15

Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met
20 25

<210> 547

<211> 58

<212> PRT

<213> Homo sapiens

<400> 547

Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu Gly Leu
5 10 15

Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala Arg Leu
20 25 30

Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His Gln Leu Cys
35 40 45

Cys Arg Met Pro Arg Thr Leu Arg Arg Leu
50 55

<210> 548

<211> 18

<212> PRT

<213> Homo sapiens

<400> 548

Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu

200

5

10

15

Glu Cys

<210> 549

<211> 18

<212> PRT

<213> Homo sapiens

<400> 549

Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg
5 10 15

Gln Ala

<210> 550

<211> 14

<212> PRT

<213> Homo sapiens

<400> 550

Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe
5 10

<210> 551

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 551

Phe Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala
1 5 10

